

Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 6, 2005, 12:45:13 / Search time 165 seconds

473,488 Million cell updates/sec

Title: US-09-856-796b-2

Sequence: 1 MATSRSTSLLAFLGCLPW.....KVFETAYQCSWESGCR 202

Scoring table:

Gapop 10.0, Expect 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing files: 45 summaries

Database:

1. A.GenSeq\_15Dec04.\*
2. geneSeq1998.\*
3. geneSeq2000.\*
4. geneSeq2001.\*
5. geneSeq2002.\*
6. geneSeq2003.\*
7. geneSeq2003b.\*
8. geneSeq2004.\*

Prod. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1047	100.0	202	3	AA093637	AA093637
2	1042	99.5	202	8	AA093637	AA093637
3	1042	99.5	202	8	AA093637	AA093637
4	1029.5	98.3	217	2	AA093637	AA093637
5	1029.5	98.3	217	2	AA093637	AA093637
6	1029.5	98.3	217	2	AA093637	AA093637
7	1029.5	98.3	217	2	AA093637	AA093637
8	1029.5	98.3	217	2	AA093637	AA093637
9	1029.5	98.3	217	2	AA093637	AA093637
10	1029.5	98.3	217	2	AA093637	AA093637
11	1028.5	98.2	217	5	AA093637	AA093637
12	1028.5	98.0	217	5	AA093637	AA093637
13	1028.5	97.9	217	5	AA093637	AA093637
14	1028.5	97.9	217	5	AA093637	AA093637
15	1028.5	97.9	217	5	AA093637	AA093637
16	1028.5	97.9	217	5	AA093637	AA093637
17	1028.5	97.9	217	5	AA093637	AA093637
18	1028.5	97.9	217	5	AA093637	AA093637
19	1024.5	97.9	217	4	AA093637	AA093637
20	1024.5	97.9	217	4	AA093637	AA093637
21	1024.5	97.9	217	4	AA093637	AA093637
22	1024.5	97.9	217	4	AA093637	AA093637
23	1024.5	97.9	217	4	AA093637	AA093637
24	1024.5	97.9	217	4	AA093637	AA093637
25	1024.5	97.9	217	4	AA093637	AA093637

26	1024.5	97.9	217	5	AA093637	AA093637
27	1024.5	97.9	217	5	AA093637	AA093637
28	1024.5	97.9	217	5	AA093637	AA093637
29	1024.5	97.9	217	5	AA093637	AA093637
30	1024.5	97.9	217	5	AA093637	AA093637
31	1024.5	97.9	217	5	AA093637	AA093637
32	1024.5	97.9	217	5	AA093637	AA093637
33	1024.5	97.9	217	5	AA093637	AA093637
34	1024.5	97.9	217	5	AA093637	AA093637
35	1024.5	97.9	217	5	AA093637	AA093637
36	1024.5	97.9	217	5	AA093637	AA093637
37	1024.5	97.9	217	5	AA093637	AA093637
38	1024.5	97.9	217	5	AA093637	AA093637
39	1024.5	97.9	217	5	AA093637	AA093637
40	1024.5	97.9	217	5	AA093637	AA093637
41	1024.5	97.9	217	5	AA093637	AA093637
42	1024.5	97.9	217	5	AA093637	AA093637
43	1024.5	97.9	217	5	AA093637	AA093637
44	1024.5	97.9	217	5	AA093637	AA093637
45	1024.5	97.9	217	5	AA093637	AA093637

ALIGNMENTS

Result 1

ID: AA093637 standard; protein, 202 AA.

AA093637

25-SEP-2000 (first entry)

Katrin acid sequence of a human growth hormone (hGH).

hGH: growth hormone; hGH: inhibitor; nuclear factor-kappaB; NF-kappaB; multi-drug resistance gene; malignant hemopathy; solid tumour; malignant blood disease; leukemias; lymphomas; solid cancer.

homo sapiens.

NC020005087-NA2.

02-JUN-2000.

24-NOV-1999: 99NO-FR002897.

25-NOV-1999: 99NO-FR002897.

(GMS) CNT NAT RECH SCT.

Hirsch P, Haeffner A;

WPI 2000-328891/3.

N-FSBR; AA06699.

Treatment of hematological or solid tumors using an inhibitor of the growth of nuclear factor-kappaB, particularly to prevent development of resistance to chemotherapeutic.

Claim 10: Page 27-28; 30pp; French.

The present sequence represents a human growth hormone (hGH). The human growth hormone protein is used as an inhibitor of nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits activation of (which contains the transcription of the multi-drug resistance gene (MDR1)).

The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins.

The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins.

The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins.

The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins.

The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins. The inhibitor is used to produce human regulatory proteins.





181. [http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=11555555](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=11555555)

RESULTS 6  
AC  
AD  
AE  
AF  
AG  
AH  
AI  
AJ  
AK  
AL  
AM  
AN  
AO  
AP  
AQ  
AR  
AS  
AT  
AU  
AV  
AW  
AX  
AY  
AZ  
BA  
BB  
BC  
BD  
BE  
BF  
BG  
BH  
BI  
BJ  
BK  
BL  
BM  
BN  
BO  
BP  
BQ  
BR  
BS  
BT  
BU  
BV  
BW  
BX  
BY  
BZ  
CA  
CB  
CC  
CD  
CE  
CF  
CG  
CH  
CI  
CJ  
CK  
CL  
CM  
CN  
CO  
CP  
CQ  
CR  
CS  
CT  
CU  
CV  
CW  
CX  
CY  
CZ  
DA  
DB  
DC  
DD  
DE  
DF  
DG  
DH  
DI  
DJ  
DK  
DL  
DM  
DN  
DO  
DP  
DQ  
DR  
DS  
DT  
DU  
DV  
DW  
DX  
DY  
DZ  
EA  
EB  
EC  
ED  
EE  
EF  
EG  
EH  
EI  
EJ  
EK  
EL  
EM  
EN  
EO  
EP  
EQ  
ER  
ES  
ET  
EU  
EV  
EW  
EX  
EY  
EZ  
FA  
FB  
FC  
FD  
FE  
FF  
FG  
FH  
FI  
FJ  
FK  
FL  
FM  
FN  
FO  
FP  
FQ  
FR  
FS  
FT  
FU  
FV  
FW  
FX  
FY  
FZ  
GA  
GB  
GC  
GD  
GE  
GF  
GG  
GH  
GI  
GJ  
GK  
GL  
GM  
GN  
GO  
GP  
GQ  
GR  
GS  
GT  
GU  
GV  
GW  
GX  
GY  
GZ  
HA  
HB  
HC  
HD  
HE  
HF  
HG  
HH  
HI  
HJ  
HK  
HL  
HM  
HN  
HO  
HP  
HQ  
HR  
HS  
HT  
HU  
HV  
HW  
HX  
HY  
HZ  
IA  
IB  
IC  
ID  
IE  
IF  
IG  
IH  
II  
IJ  
IK  
IL  
IM  
IN  
IO  
IP  
IQ  
IR  
IS  
IT  
IU  
IV  
IW  
IX  
IY  
IZ  
JA  
JB  
JC  
JD  
JE  
JF  
JG  
JH  
JI  
JJ  
JK  
JL  
JM  
JN  
JO  
JP  
JQ  
JR  
JS  
JT  
JU  
JV  
JW  
JX  
JY  
JZ  
KA  
KB  
KC  
KD  
KE  
KF  
KG  
KH  
KI  
KJ  
KK  
KL  
KM  
KN  
KO  
KP  
KQ  
KR  
KS  
KT  
KU  
KV  
KW  
KX  
KY  
KZ  
LA  
LB  
LC  
LD  
LE  
LF  
LG  
LH  
LI  
LJ  
LK  
LM  
LN  
LO  
LP  
LQ  
LR  
LS  
LT  
LU  
LV  
LW  
LX  
LY  
LZ  
MA  
MB  
MC  
MD  
ME  
MF  
MG  
MH  
MI  
MJ  
MK  
ML  
MM  
MN  
MO  
MP  
MQ  
MR  
MS  
MT  
MU  
MV  
MW  
MX  
MY  
MZ  
NA  
NB  
NC  
ND  
NE  
NF  
NG  
NH  
NI  
NJ  
NK  
NL  
NM  
NN  
NO  
NP  
NQ  
NR  
NS  
NT  
NU  
NV  
NW  
NX  
NY  
NZ  
OA  
OB  
OC  
OD  
OE  
OF  
OG  
OH  
OI  
OJ  
OK  
OL  
OM  
ON  
OO  
OP  
OQ  
OR  
OS  
OT  
OU  
OV  
OW  
OX  
OY  
OZ  
PA  
PB  
PC  
PD  
PE  
PF  
PG  
PH  
PI  
PJ  
PK  
PL  
PM  
PN  
PO  
PP  
PQ  
PR  
PS  
PT  
PU  
PV  
PW  
PX  
PY  
PZ  
QA  
QB  
QC  
QD  
QE  
QF  
QG  
QH  
QI  
QJ  
QK  
QL  
QM  
QN  
QO  
QP  
QQ  
QR  
QS  
QT  
QU  
QV  
QW  
QX  
QY  
QZ  
RA  
RB  
RC  
RD  
RE  
RF  
RG  
RH  
RI  
RJ  
RK  
RL  
RM  
RN  
RO  
RP  
RQ  
RR  
RS  
RT  
RU  
RV  
RW  
RX  
RY  
RZ  
SA  
SB  
SC  
SD  
SE  
SF  
SG  
SH  
SI  
SJ  
SK  
SL  
SM  
SN  
SO  
SP  
SQ  
SR  
SS  
ST  
SU  
SV  
SW  
SX  
SY  
SZ  
TA  
TB  
TC  
TD  
TE  
TF  
TG  
TH  
TI  
TJ  
TK  
TL  
TM  
TN  
TO  
TP  
TQ  
TR  
TS  
TT  
TU  
TV  
TW  
TX  
TY  
TZ  
UA  
UB  
UC  
UD  
UE  
UF  
UG  
UH  
UI  
UJ  
UK  
UL  
UM  
UN  
UO  
UP  
UQ  
UR  
US  
UT  
UU  
UV  
UW  
UX  
UY  
UZ  
VA  
VB  
VC  
VD  
VE  
VF  
VG  
VH  
VI  
VJ  
VK  
VL  
VM  
VN  
VO  
VP  
VQ  
VR  
VS  
VT  
VU  
VV  
VW  
VX  
VY  
VZ  
WA  
WB  
WC  
WD  
WE  
WF  
WG  
WH  
WI  
WJ  
WK  
WL  
WM  
WN  
WO  
WP  
WQ  
WR  
WS  
WT  
WU  
WV  
WW  
WX  
WY  
WZ  
XA  
XB  
XC  
XD  
XE  
XF  
XG  
XH  
XI  
XJ  
XK  
XL  
XM  
XN  
XO  
XP  
XQ  
XR  
XS  
XT  
XU  
XV  
XW  
XX  
XY  
XZ  
YA  
YB  
YC  
YD  
YE  
YF  
YG  
YH  
YI  
YJ  
YK  
YL  
YM  
YN  
YO  
YP  
YQ  
YR  
YS  
YT  
YU  
YV  
YW  
YX  
YY  
YZ  
ZA  
ZB  
ZC  
ZD  
ZE  
ZF  
ZG  
ZH  
ZI  
ZJ  
ZK  
ZL  
ZM  
ZN  
ZO  
ZP  
ZQ  
ZR  
ZS  
ZT  
ZU  
ZV  
ZW  
ZX  
ZY  
ZZ

181. [http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=11555555](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=11555555)

RESULTS 6  
AC  
AD  
AE  
AF  
AG  
AH  
AI  
AJ  
AK  
AL  
AM  
AN  
AO  
AP  
AQ  
AR  
AS  
AT  
AU  
AV  
AW  
AX  
AY  
AZ  
BA  
BB  
BC  
BD  
BE  
BF  
BG  
BH  
BI  
BJ  
BK  
BL  
BM  
BN  
BO  
BP  
BQ  
BR  
BS  
BT  
BU  
BV  
BW  
BX  
BY  
BZ  
CA  
CB  
CC  
CD  
CE  
CF  
CG  
CH  
CI  
CJ  
CK  
CL  
CM  
CN  
CO  
CP  
CQ  
CR  
CS  
CT  
CU  
CV  
CW  
CX  
CY  
CZ  
DA  
DB  
DC  
DD  
DE  
DF  
DG  
DH  
DI  
DJ  
DK  
DL  
DM  
DN  
DO  
DP  
DQ  
DR  
DS  
DT  
DU  
DV  
DW  
DX  
DY  
DZ  
EA  
EB  
EC  
ED  
EE  
EF  
EG  
EH  
EI  
EJ  
EK  
EL  
EM  
EN  
EO  
EP  
EQ  
ER  
ES  
ET  
EU  
EV  
EW  
EX  
EY  
EZ  
FA  
FB  
FC  
FD  
FE  
FF  
FG  
FH  
FI  
FJ  
FK  
FL  
FM  
FN  
FO  
FP  
FQ  
FR  
FS  
FT  
FU  
FV  
FW  
FX  
FY  
FZ  
GA  
GB  
GC  
GD  
GE  
GF  
GG  
GH  
GI  
GJ  
GK  
GL  
GM  
GN  
GO  
GP  
GQ  
GR  
GS  
GT  
GU  
GV  
GW  
GX  
GY  
GZ  
HA  
HB  
HC  
HD  
HE  
HF  
HG  
HH  
HI  
HJ  
HK  
HL  
HM  
HN  
HO  
HP  
HQ  
HR  
HS  
HT  
HU  
HV  
HW  
HX  
HY  
HZ  
IA  
IB  
IC  
ID  
IE  
IF  
IG  
IH  
II  
IJ  
IK  
IL  
IM  
IN  
IO  
IP  
IQ  
IR  
IS  
IT  
IU  
IV  
IW  
IX  
IY  
IZ  
JA  
JB  
JC  
JD  
JE  
JF  
JG  
JH  
JI  
JJ  
JK  
JL  
JM  
JN  
JO  
JP  
JQ  
JR  
JS  
JT  
JU  
JV  
JW  
JX  
JY  
JZ  
KA  
KB  
KC  
KD  
KE  
KF  
KG  
KH  
KI  
KJ  
KK  
KL  
KM  
KN  
KO  
KP  
KQ  
KR  
KS  
KT  
KU  
KV  
KW  
KX  
KY  
KZ  
LA  
LB  
LC  
LD  
LE  
LF  
LG  
LH  
LI  
LJ  
LK  
LM  
LN  
LO  
LP  
LQ  
LR  
LS  
LT  
LU  
LV  
LW  
LX  
LY  
LZ  
MA  
MB  
MC  
MD  
ME  
MF  
MG  
MH  
MI  
MJ  
MK  
ML  
MM  
MN  
MO  
MP  
MQ  
MR  
MS  
MT  
MU  
MV  
MW  
MX  
MY  
MZ  
NA  
NB  
NC  
ND  
NE  
NF  
NG  
NH  
NI  
NJ  
NK  
NL  
NM  
NN  
NO  
NP  
NQ  
NR  
NS  
NT  
NU  
NV  
NW  
NX  
NY  
NZ  
OA  
OB  
OC  
OD  
OE  
OF  
OG  
OH  
OI  
OJ  
OK  
OL  
OM  
ON  
OO  
OP  
OQ  
OR  
OS  
OT  
OU  
OV  
OW  
OX  
OY  
OZ  
PA  
PB  
PC  
PD  
PE  
PF  
PG  
PH  
PI  
PJ  
PK  
PL  
PM  
PN  
PO  
PP  
PQ  
PR  
PS  
PT  
PU  
PV  
PW  
PX  
PY  
PZ  
QA  
QB  
QC  
QD  
QE  
QF  
QG  
QH  
QI  
QJ  
QK  
QL  
QM  
QN  
QO  
QP  
QQ  
QR  
QS  
QT  
QU  
QV  
QW  
QX  
QY  
QZ  
RA  
RB  
RC  
RD  
RE  
RF  
RG  
RH  
RI  
RJ  
RK  
RL  
RM  
RN  
RO  
RP  
RQ  
RR  
RS  
RT  
RU  
RV  
RW  
RX  
RY  
RZ  
SA  
SB  
SC  
SD  
SE  
SF  
SG  
SH  
SI  
SJ  
SK  
SL  
SM  
SN  
SO  
SP  
SQ  
SR  
SS  
ST  
SU  
SV  
SW  
SX  
SY  
SZ  
TA  
TB  
TC  
TD  
TE  
TF  
TG  
TH  
TI  
TJ  
TK  
TL  
TM  
TN  
TO  
TP  
TQ  
TR  
TS  
TT  
TU  
TV  
TW  
TX  
TY  
TZ  
UA  
UB  
UC  
UD  
UE  
UF  
UG  
UH  
UI  
UJ  
UK  
UL  
UM  
UN  
UO  
UP  
UQ  
UR  
US  
UT  
UU  
UV  
UW  
UX  
UY  
UZ  
VA  
VB  
VC  
VD  
VE  
VF  
VG  
VH  
VI  
VJ  
VK  
VL  
VM  
VN  
VO  
VP  
VQ  
VR  
VS  
VT  
VU  
VV  
VW  
VX  
V







completes comparing the nucleotide sequence of GH1 gene obtained from the patient sample with a standard human GH1 gene sequence in order to identify any variation (GH1 variant). The method is useful in screening patients for growth hormone irregularities, especially detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in identifying the etiology of GH deficiency, such as diabetes, obesity, binding defects and enzyme/acromy or gigantism conditions associated with acromegaly, acromegaly, lipolytic and protein anabolic defects, conditions associated with sodium and water balance dysfunction and syndromes, mood and sleep defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH1 variant sequence is useful in gene therapy or protein therapy. The GH1 or GH1 variant sequence can be used in the preparation of a medication, advantage of: expanding the use of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying of GH1 gene mutations in the etiology of short stature; evaluation and development of rapid the structure and function of GH1 molecule and development of rapid the structure and function of GH1 molecule. This sequence is a variant of human growth hormone 1 (GH1); one of many variations of GH1 does not appear in the method of the invention. The GH1 variant sequence is sequence (A00119) given in figure 6

Sequence 217 Aa:

Query Match: 98.4%; Score 1026.5; DB 5; Length 217;

Best Local Similarity: 92.6%; Pred. No. 1.7e-87; Indels 15; Gaps 1;

Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 WATGRTSLLAFLQCLCMWQGSAPFPIPLSPNNISAPAHRIHQAIAPTGTF-- 57  
1 WATGRTSLLAFLQCLCMWQGSAPFPIPLSPNNISAPAHRIHQAIAPTGTF-- 57  
58 -----NQGISCFRESIPFSNENETQKSNIELAISLILQSNLEPQVRA 105  
61 VYPSNLSVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 165  
106 VYPSNLSVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 165  
121 SPVNSLVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 180  
166 ALMDYGLCYFRQMDQVTFPIALVQCSVSGSCF 202  
181 ALMDYGLCYFRQMDQVTFPIALVQCSVSGSCF 217

RESULT 12

A0011746 standard protein, 217 Aa.

ID A0011746;

NC A0011746;

12-NBR-2002 (first entry)

DB Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

XX Growth hormone 1 gene (GH1), K19A mutant.

15-NOV-2001.  
14-MAY-2001, 2001 NC-0800126.  
12-MAY-2001, 2000CB-0001155.  
14-JULY-2000, 2000CB-0030604.  
(UWMA-) UNIV MILES COLLEGE OF MEDICINE.  
Cooper NH, Proctor M, Gregory J, Miller DB;  
NRI: 2002-08978/12.  
Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, especially detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in identifying the etiology of GH deficiency, such as diabetes, obesity, binding defects and enzyme/acromy or gigantism conditions associated with acromegaly, acromegaly, lipolytic and protein anabolic defects, conditions associated with sodium and water balance dysfunction and syndromes, mood and sleep defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH1 variant sequence is useful in gene therapy or protein therapy. The GH1 or GH1 variant sequence can be used in the preparation of a medication, advantage of: expanding the use of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying of GH1 gene mutations in the etiology of short stature; evaluation and development of rapid the structure and function of GH1 molecule and development of rapid the structure and function of GH1 molecule. This sequence is a variant of human growth hormone 1 (GH1); one of many variations of GH1 does not appear in the method of the invention. The GH1 variant sequence is sequence (A00119) given in figure 6

Query Match: 98.4%; Score 1026.5; DB 5; Length 217;

Best Local Similarity: 92.6%; Pred. No. 2.8e-87; Indels 15; Gaps 1;

Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 WATGRTSLLAFLQCLCMWQGSAPFPIPLSPNNISAPAHRIHQAIAPTGTF-- 57  
1 WATGRTSLLAFLQCLCMWQGSAPFPIPLSPNNISAPAHRIHQAIAPTGTF-- 57  
58 -----NQGISCFRESIPFSNENETQKSNIELAISLILQSNLEPQVRA 105  
61 VYPSNLSVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 165  
106 VYPSNLSVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 165  
121 SPVNSLVYGASNSVVDLQKDEIGTQVMELEPSGSPRTQIPQTSKEDNSND 180  
166 ALMDYGLCYFRQMDQVTFPIALVQCSVSGSCF 202  
181 ALMDYGLCYFRQMDQVTFPIALVQCSVSGSCF 217

RESULT 13

XX Key

XX Key

XX Key

XX Key





investigation, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in the diagnosis of GH deficiency, and in the identification of patients with therapeutic, diagnostic or detection method, patients with diabetes, obesity binding defects and sleeping apnoea, or gigantism conditions associated with acromegaly, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and potassium GH dysfunction and syndromes, mood and sleep defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant can be used in the preparation of a medicament advantage of: expanding the knowledge of GH gene mutations; evaluating the role of GH gene mutations in the etiology of short stature; identifying the role of GH gene mutations in the etiology of short stature; evaluation of the role of GH gene mutations in the etiology of short stature; evaluation of the role of GH gene mutations in the etiology of short stature. This sequence is a variant of the structure and function of GH1, one of many variations of the GH1 gene of human growth hormone 1 (GH1), one of many variations of the GH1 gene discussed in the method of the invention, can be created from the GH1 wild type sequence (AB011119) given in Figure 6

Query March 97.98; score 1025.5; DB 5; Length 217;

Best local similarity 92.6%; Pred. No. 3.3e-87; Indels 15; Gaps 1;

Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 MANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
1 VANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
1 VANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
58 -----NQTSLCFRSETPFRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
106 SVFPAHSLVYGAGSNVYLLKQLEGGTQWLRLEDSRPTQVFPQYTSFNTNSND 165  
121 SVFPAHSLVYGAGSNVYLLKQLEGGTQWLRLEDSRPTQVFPQYTSFNTNSND 180  
166 ALMAYGGLYCRKDKDVFETPLAVQCSVSCGF 202  
181 ALMAYGGLYCRKDKDVFETPLAVQCSVSCGF 217

RESULT 15

AAD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

12-MAY-2001; 200GB-00011459.  
14-JUL-2001; 200GB-00306004.  
(UNM-) UNIV MARYLAND COLLEGE OF MEDICINE.  
Cooper DM, Proctor MW, Gregory J, Miller DB,  
WPI 2002-089798/12.  
Detecting growth hormone variants (GH1), useful in screening patients for growth hormone deficiency, and in the identification of patients with therapeutic, diagnostic or detection method, patients with diabetes, obesity binding defects and sleeping apnoea, or gigantism conditions associated with acromegaly, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and potassium GH dysfunction and syndromes, mood and sleep defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant can be used in the preparation of a medicament advantage of: expanding the knowledge of GH gene mutations; evaluating the role of GH gene mutations in the etiology of short stature; identifying the role of GH gene mutations in the etiology of short stature; evaluation of the role of GH gene mutations in the etiology of short stature; evaluation of the role of GH gene mutations in the etiology of short stature. This sequence is a variant of the structure and function of GH1, one of many variations of the GH1 gene of human growth hormone 1 (GH1), one of many variations of the GH1 gene discussed in the method of the invention, can be created from the GH1 wild type sequence (AB011119) given in Figure 6

Query March 97.98; score 1025.5; DB 5; Length 217;

Best local similarity 92.6%; Pred. No. 3.3e-87; Indels 15; Gaps 1;

Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

1 MANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
1 VANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
1 VANGSRSTLLAFGLCLMPCGSGAPPTPLPRFPAHARHQAAPPTQGE-- 57  
58 -----NQTSLCFRSETPFRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
61 VPEKQSTPLQNVYLSFCSFSPRSEETQPSNELAISLLIGMPEVQTA 105  
106 SVFPAHSLVYGAGSNVYLLKQLEGGTQWLRLEDSRPTQVFPQYTSFNTNSND 165  
121 SVFPAHSLVYGAGSNVYLLKQLEGGTQWLRLEDSRPTQVFPQYTSFNTNSND 180  
166 ALMAYGGLYCRKDKDVFETPLAVQCSVSCGF 202  
181 ALMAYGGLYCRKDKDVFETPLAVQCSVSCGF 217

RESULT 15

AAD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

AD11744 standard protein: 217 AA.

Search completed: February 6, 2005, 13:01:28  
Job time: 167 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using SW model

Run on: February 6, 2005, 12:45:33 / Search time 174 Seconds

Title: US-09-856-796d-2  
Perfect score: 1047  
Sequence: 1 MATKSRISLLANPLCLP.....KVFPLAIQGSQVDSQCF 202  
5941483, Million cells updated/sec

Scoring table:  
RUSING2  
dappo 10.0, Gapset 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing files: 45 summaries

Database:

1: uniprot\_sprot.\*

2: uniprot\_crem.\*

Print: No. is the number of results predicted by chance to have a grade greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1047	100	216	1	SOVA_HUMAN
2	1020.5	97.3	217	1	SOVA_HUMAN
3	1018.5	97.3	217	1	SOVA_HUMAN
4	1018.5	97.3	217	1	SOVA_HUMAN
5	957	91.4	217	1	SOVA_HUMAN
6	957	91.4	217	1	SOVA_HUMAN
7	955.5	91.3	217	1	SOVA_HUMAN
8	945.5	90.3	217	1	SOVA_HUMAN
9	945.5	90.3	217	1	SOVA_HUMAN
10	931.5	89.7	217	1	SOVA_HUMAN
11	908.5	86.8	217	1	SOVA_HUMAN
12	904.5	86.4	217	1	SOVA_HUMAN
13	892.5	84.3	217	1	SOVA_HUMAN
14	882.5	83.3	217	1	SOVA_HUMAN
15	870.5	83.1	217	1	SOVA_HUMAN
16	870.5	83.1	217	1	SOVA_HUMAN
17	855.5	81.7	217	1	SOVA_HUMAN
18	855.5	81.7	217	1	SOVA_HUMAN
19	833.5	81.2	217	1	SOVA_HUMAN
20	833.5	81.2	217	1	SOVA_HUMAN
21	829.5	79.4	217	1	SOVA_HUMAN
22	829.5	79.4	217	1	SOVA_HUMAN
23	779.5	74.5	217	1	SOVA_HUMAN
24	779.5	74.5	217	1	SOVA_HUMAN
25	754.5	72.1	217	1	SOVA_HUMAN
26	754.5	72.1	217	1	SOVA_HUMAN
27	726.5	69.4	216	1	SOVA_HUMAN
28	702	67.0	216	1	SOVA_HUMAN
29	701	67.0	216	1	SOVA_HUMAN
30	701	67.0	216	1	SOVA_HUMAN
31	696	66.5	216	1	SOVA_HUMAN

## ALIGNMENTS

## RESULT 1

## SOVA\_HUMAN

## STANDARD

## PRT, 217 AA.

## DT 21-02-1992 (Ref. 21, last sequence update)

## DT 01-MAR-1992 (Ref. 21, last sequence update)

## DT 25-OCT-2004 (Ref. 45, last annotation update)

## DB human (growth hormone)

## Name: GH1

## Accession: P01246

## Description: Growth hormone

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246

## Accession: P01246





RESULT 4  
 AC O61970 PRELIMINARY; PRT: 217 AA.  
 AC O61970 (TRIMBLER); 27 Created  
 DT 05-JUN-2004 (TRIMBLER); 27 Last sequence update  
 DT 05-JUN-2004 (TRIMBLER); 27 Last annotation update  
 CC Growth hormone 1 variant 2.  
 CC Homo sapiens (Human).  
 CC Eukaryotes; Metazoa; Chordata; Vertebrates; Buteleostomi;  
 CC Mammalia; Eutheria; Primates; Carnivora; Nonartiodactyla; Homio-  
 CC \_Mammalia-99491.  
 CC [1]  
 SEQUENCE FROM N.A.  
 RA JORGE A.M., ANDRIOLLO J.P., MORGANO M.B.,  
 RA BERNARDINI L., ANDRIOLLO L. The EMBL/GenBank/DBJ databases.  
 RA EMBL; A613432; A611059.1;  
 RA HSP; P01213; IAXI.  
 RA GO; GO:0003179, F-hormone activity; IAX.  
 RA Interpro; IPR001400, Somatotropin.  
 RA Interpro; IPR009079, 4\_helix\_cytokine.  
 RA PRINTS; PR00266; SOMATOTROPIN.  
 RA PROSITE; PS00266; SOMATOTROPIN 1, 1.  
 RA PROSITE; PS00338; SOMATOTROPIN 2, 1.  
 SO SEQUENCE; 217 AA; 2456 MW; 120079523DB51A CMC64;  
 Query Match 92.1%; Score 106.5; DB 2; Length 217;  
 Best Local Similarity 92.2%; Pred. No. 4,6e-84; Indels 15; Gaps 1;  
 Matchee 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;  
 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE--- 57  
 DB 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE 60  
 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 OV 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 DB 61 VYPRKQKSTFQVQGLQVPSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 120  
 OV 106 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 165  
 DB 121 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 180  
 OV 166 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 202  
 DB 161 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 217  
 RESULT 5  
 AC O61970 PRELIMINARY; PRT: 217 AA.  
 AC P310931 (REL; 37, Created)  
 DT 01-OCT-1993 (REL; 37, Sequence update)  
 DT 05-JUN-2004 (REL; 45, Last annotation update)  
 CC Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth  
 CC hormone) (Growth hormone 1).  
 CC Macaca mulatta (Rhesus macaque).  
 CC Eukaryotes; Metazoa; Chordata; Vertebrates; Buteleostomi;  
 CC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;  
 CC Cercopithecoidea; Macaca.  
 CC NCBI Taxid=9544.  
 CC [1]  
 SEQUENCE FROM N.A.  
 RA JORGE A.M., ANDRIOLLO J.P., MORGANO M.B.,  
 RA BERNARDINI L., ANDRIOLLO L. The EMBL/GenBank/DBJ databases.  
 RA EMBL; A613432; A611059.1;  
 RA HSP; P01213; IAXI.  
 RA GO; GO:0003179, F-hormone activity; IAX.  
 RA Interpro; IPR001400, Somatotropin.  
 RA Interpro; IPR009079, 4\_helix\_cytokine.  
 RA PRINTS; PR00266; SOMATOTROPIN.  
 RA PROSITE; PS00266; SOMATOTROPIN 1, 1.  
 RA PROSITE; PS00338; SOMATOTROPIN 2, 1.  
 SO SEQUENCE; 217 AA; 2456 MW; 120079523DB51A CMC64;  
 Query Match 92.1%; Score 98.1; DB 1; Length 217;  
 Best Local Similarity 88.9%; Pred. No. 6,6e-81;  
 Matchee 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;  
 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE--- 57  
 DB 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE 60  
 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 OV 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 DB 61 VYPRKQKSTFQVQGLQVPSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 120  
 OV 106 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 165  
 DB 121 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 180  
 OV 166 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 202  
 DB 161 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 217  
 RESULT 6  
 AC O64643 PRELIMINARY; PRT: 202 AA.  
 AC O64643 (TRIMBLER); 05, Created  
 DT 01-JAN-1998 (TRIMBLER); 05, Last sequence update  
 DT 01-MAR-2004 (TRIMBLER); 26, Last annotation update  
 CC Growth hormone 2ndb secretin precursor.  
 CC Homo sapiens (Human).  
 CC [1]

Endocrinology 133:1744-1752(1993).  
 [12]  
 SEQUENCE OF 217-217.  
 RA JORGE A.M., ANDRIOLLO J.P., MORGANO M.B.,  
 RA BERNARDINI L., ANDRIOLLO L. The EMBL/GenBank/DBJ databases.  
 RA EMBL; A613432; A611059.1;  
 RA HSP; P01213; IAXI.  
 RA GO; GO:0003179, F-hormone activity; IAX.  
 RA Interpro; IPR001400, Somatotropin.  
 RA Interpro; IPR009079, 4\_helix\_cytokine.  
 RA PRINTS; PR00266; SOMATOTROPIN.  
 RA PROSITE; PS00266; SOMATOTROPIN 1, 1.  
 RA PROSITE; PS00338; SOMATOTROPIN 2, 1.  
 SO SEQUENCE; 217 AA; 2456 MW; 120079523DB51A CMC64;  
 Query Match 92.1%; Score 98.1; DB 1; Length 217;  
 Best Local Similarity 88.9%; Pred. No. 6,6e-81;  
 Matchee 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;  
 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE--- 57  
 DB 1 MATGSRTELALVGLCLPMVGSSAFPTTSLRFLNNAFAARHQLAATPTQGE 60  
 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 OV 58 -----HPPTGLPSSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 105  
 DB 61 VYPRKQKSTFQVQGLQVPSRPTPSNNEETQKSNLEALSLTLOMLSPVOTLA 120  
 OV 106 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 165  
 DB 121 SVFANVLYGASGVDTLALDEGLTLMGRIDDSRSRTQVFPQVTSLEFNSHND 180  
 OV 166 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 202  
 DB 161 ALNANYGLVCFKRMQKVFATFATVQSGVSGCF 217  
 RESULT 6  
 AC O64643 PRELIMINARY; PRT: 202 AA.  
 AC O64643 (TRIMBLER); 05, Created  
 DT 01-JAN-1998 (TRIMBLER); 05, Last sequence update  
 DT 01-MAR-2004 (TRIMBLER); 26, Last annotation update  
 CC Growth hormone 2ndb secretin precursor.  
 CC Homo sapiens (Human).  
 CC [1]









```

DT      05-JUN-2004 (Rel. 4.4). Last annotation update)
DR      Somatotropin precursor (growth hormone).
CC      [1] PubMed=94803
OC      Callicebus jacchus (Common marmoset).
OC      Suayutzi's Marmoset (Chondrus Canaliculus).
OC      Mammalia; Anthropoidea; Primates; Platyrrhini; Callitrichidae; Callithrix.
PA      [1] TaxID=94803
RA      SEQUENCE FROM N.A.:
RA      Wallis O.C., Wallis J.N.: Isolation of a putative growth hormone encoding
RT      gene from the marmoset (Callicebus jacchus).4
RL      Submitted (JAN-2000) to the EMBL/GenBank/TrEMBL databases. Its major
CC      FUNCTION: plays an important role in stimulating the liver and
CC      other tissues to secrete IGF-I. It stimulates both the
CC      differentiation and proliferation of myoblasts. It also stimulates
CC      amino acid uptake and protein synthesis in muscle and other
CC      tissues.
CC      -1- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC      -1- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC      This SwissProt entry has copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      at the European Bioinformatics Institute. There are no restrictions on what
CC      can be done with this information as long as usage by and for commercial
CC      entities is acknowledged. The copyright notice is included in the file
CC      modified and sent to a license agreement (see http://www.ebi.ac.uk/announcements)
CC      or send an email to license@ebi.slb.ch.
CC      CC
CC      BMRB: P01243, C003681.1...
DR      InterPro: IPRO00079; 4_helix_cytokine.
DR      InterPro: IPRO001400; Somatotropin.
DR      Pfam: PF00286; SOMATOTROPIN.
DR      PROSITE: PS00286; SOMATOTROPIN_1.
DR      PROSITE: PS00338; SOMATOTROPIN_2.
NR      Homolog: Pituitary; 26 aa. By similarity.
NR      Homolog: Pituitary; 26 aa. By similarity.
NR      CHAIN: 79 191. Somatotropin.
FT      DISULFID 208 217. By similarity.
FT      DISULFID 218 219. By similarity.
DS      SOURCEID 217 AA, 20959 MW, EI0251A127E612 CNOG4;

Query Match      85.5% Score 895.5; DG 1; Length 217;
Batch local identity 11; Mismatches 15; Gaps 1
Machina 16; Conservative 11; Miscellaneous 15; Indels 15; Gaps 1
OY      1 WATGTSSTSLALGLQLPLWQDGSNPFPTLSLPPNALSNNPFGVAGAAKQGP--- 57
DB      1 WAKGSSSTSLALGLQLPLWQDGSNPFPTLSLPPNALSNNPFGVAGAAKQGP--- 57
OY      58 -----HPGTSLPSSTLPFSNKETPEQNNSNLKLAISLLTGRN ENPKRFA 100
DB      58 -----HPGTSLPSSTLPFSNKETPEQNNSNLKLAISLLTGRN ENPKRFA 100
OY      4 YIRKQKSTFLQNGVYLVADLKLDESGTQMTLELDSDSPQTQIPACTISKTFSTNDG 120
DB      4 YIRKQKSTFLQNGVYLVADLKLDESGTQMTLELDSDSPQTQIPACTISKTFSTNDG 120
OY      121 SYFNALLIVSVDSDSVLRDLGGEDITQMLLDDSDSFQIFDKTKFVSQND 184
DB      121 SYFNALLIVSVDSDSVLRDLGGEDITQMLLDDSDSFQIFDKTKFVSQND 184
OY      166 ALLNQTLQLCFRRQKNVFETFLAVQASVYSAGSQ 202
DB      166 ALLNQTLQLCFRRQKNVFETFLAVQASVYSAGSQ 202
OY      181 ALLNQTLQLCFRRQKNVFETFLAVQASVYSAGSQ 217
DB      181 ALLNQTLQLCFRRQKNVFETFLAVQASVYSAGSQ 217

RESULT 14
OSEQID    PRELIMINARY; PRF: 217 AA.
AC         Q886U1;
DT 01-JUN-2003 (TRFBIgnr1, 24, Created)
DT 01-JUN-2003 (TRFBIgnr1, 26, Last annotation update)
DT 01-JUN-2004 (TRFBIgnr1, 26, Last annotation update)

```



Page 10

```

0Y 1 MARGSTELLALFOLLICLPMJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---5
0Y 1 MARGSTELLALFOLLICLPMJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---5
Db 1 MARGSTELLALFOLLICLPMJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---60
0Y -----MPCSTLCEBSIFPPSNHETQOQSNLJLJLJLJGSMLEWQJFLA 105
Db -----MPCSTLCEBSIFPPSNHETQOQSNLJLJLJLJGSMLEWQJFLA 120
0Y 61 YIPKQWTFJHDSOTSCFCSJIPFSPNHWETQOQSNLJLJLJLJHSMLEWQJFLA 120
Db 61 YIPKQWTFJHDSOTSCFCSJIPFSPNHWETQOQSNLJLJLJLJHSMLEWQJFLA 120
0Y 106 SVFANSLVQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---165
Db 106 SVFANSLVQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---165
0Y 121 GPNANNUYVJHDSOTSCFCSJIPFSPNHWETQOQSNLJLJLJLJHSMLEWQJFLA 180
Db 121 GPNANNUYVJHDSOTSCFCSJIPFSPNHWETQOQSNLJLJLJLJHSMLEWQJFLA 180
0Y 166 ALJANNGVJLVCYPRJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---202
Db 166 ALJANNGVJLVCYPRJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---202
0Y 181 ALJANNGVJLVCYPRJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---217
Db 181 ALJANNGVJLVCYPRJQJGSAEPFIPASLPLNBSJLJMHJHQAADTQJGZ---217

```

























***This Page Blank (uspto)***



GenScope version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

ON protein - protein search, using sw model

Run on: February 6, 2005, 12:55:23 / Search time 40 seconds

Title: US-09-856-796b-2  
Sequence: 1 MANSERSLALAFCLLPM.....KMTETATVQASVRSRSC 202  
485,995 Million cells updated/sec

Scoring table: BLOSUM62

Deposited: 10.0, Gapenc 0.5

Searched: 289416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 293416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

Database:

1: P131.\*

2: P131.\*

3: P131.\*

4: P131.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the observed score.  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Match	Length	DB ID	Description
1	1024.5	97.9	217	1 STPH	somatotropin - pre
2	981.5	93.7	217	2 167410	somatotropin - pre
3	871.5	88.7	217	1 STPH	somatotropin - pre
4	872.5	88.3	217	1 LQD05	somatotropin - pre
5	865.5	82.8	217	2 167409	somatotropin - pre
6	865.5	81.2	217	2 152457	somatotropin - pre
7	843.5	80.5	215	2 A5443	somatotropin - pre
8	843.5	80.5	215	2 A5443	somatotropin - pre
9	843.5	80.5	215	2 A5443	somatotropin - pre
10	811.5	79.4	212	2 167408	somatotropin - pre
11	798.5	74.5	199	2 B1435	somatotropin - pre
12	798.5	74.5	199	2 B1435	somatotropin - pre
13	694.5	66.3	216	1 STPH	somatotropin - pre
14	687.5	65.6	216	2 A5443	somatotropin - pre
15	687.5	65.6	216	2 A5443	somatotropin - pre
16	682.5	65.1	216	2 A5443	somatotropin - pre
17	679.5	64.9	216	1 STPH	somatotropin - pre
18	677.5	64.7	217	1 STPH	somatotropin - pre
19	677.5	64.7	217	1 STPH	somatotropin - pre
20	666.5	63.2	216	2 A5443	somatotropin - pre
21	666.5	63.2	217	1 STPH	somatotropin - pre
22	666.5	63.2	217	2 A5443	somatotropin - pre
23	666.5	63.2	217	2 A5443	somatotropin - pre
24	654.5	58.4	216	1 STPH	somatotropin - pre
25	602.5	57.5	190	2 P10219	somatotropin - pre
26	602.5	57.5	190	2 P10219	somatotropin - pre
27	598.5	57.4	190	1 A61584	somatotropin - pre
28	598.5	57.4	190	1 A61584	somatotropin - pre
29	596.5	56.9	190	1 STPH	somatotropin - pre

## ALIGNMENTS

### SUMMARY

1: somatotropin I precursor (validated) - human  
2: somatotropin I precursor (validated) - human  
3: somatotropin I precursor (validated) - human  
4: somatotropin I precursor (validated) - human  
5: somatotropin I precursor (validated) - human  
6: somatotropin I precursor (validated) - human  
7: somatotropin I precursor (validated) - human  
8: somatotropin I precursor (validated) - human  
9: somatotropin I precursor (validated) - human  
10: somatotropin I precursor (validated) - human  
11: somatotropin I precursor (validated) - human  
12: somatotropin I precursor (validated) - human  
13: somatotropin I precursor (validated) - human  
14: somatotropin I precursor (validated) - human  
15: somatotropin I precursor (validated) - human  
16: somatotropin I precursor (validated) - human  
17: somatotropin I precursor (validated) - human  
18: somatotropin I precursor (validated) - human  
19: somatotropin I precursor (validated) - human  
20: somatotropin I precursor (validated) - human  
21: somatotropin I precursor (validated) - human  
22: somatotropin I precursor (validated) - human  
23: somatotropin I precursor (validated) - human  
24: somatotropin I precursor (validated) - human  
25: somatotropin I precursor (validated) - human  
26: somatotropin I precursor (validated) - human  
27: somatotropin I precursor (validated) - human  
28: somatotropin I precursor (validated) - human  
29: somatotropin I precursor (validated) - human







A/Cross-references: UNIPROT:Q07367; GB:U16555; NID:9293112; PIR:AA18841.1; PID:9293114  
Cisfamily: prolactin

Query Match 82.6% Score 86.5; DB 2; Length 217;  
Best Local Similarity 77.4% Pct. Ident. 15;

Matches 168; Conservative 14; Mismatches 20; Indels 15; Gaps 1;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
181 SLNNTVQLCFKDKMNVETPTLALVQCSVSGCF 217

## RESULT 7

Chorionic gonadotropin-1 - rhesus macaque  
C/Spectat: Macaca mulatta  
C/Date: 31-May-1996 Sequence revision 1; May-1996 ktext\_change 09-Jul-2004

A/Cross-references: UNIPROT:Q07367; GB:U16552; NID:9293108; PIR:AA18892.1; PID:9293106  
Cisfamily: prolactin

Query Match 81.2% Score 85.0; DB 2; Length 217;  
Best Local Similarity 75.6% Pct. Ident. 15;

Matches 164; Conservative 18; Mismatches 20; Indels 15; Gaps 1;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
181 SLNNTVQLCFKDKMNVETPTLALVQCSVSGCF 217

## RESULT 8

Chorionic gonadotropin - rhesus macaque  
C/Spectat: Macaca mulatta  
C/Date: 31-May-1996 Sequence revision 1; May-1996 ktext\_change 09-Jul-2004

A/Cross-references: UNIPROT:Q07367; GB:U16552; NID:9293108; PIR:AA18892.1; PID:9293106  
Cisfamily: prolactin

Query Match 80.5% Score 84.5; DB 2; Length 217;  
Best Local Similarity 75.6% Pct. Ident. 15;

Matches 164; Conservative 18; Mismatches 20; Indels 15; Gaps 1;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
181 SLNNTVQLCFKDKMNVETPTLALVQCSVSGCF 217

## RESULT 9

Chorionic gonadotropin - rhesus macaque  
C/Spectat: Macaca mulatta  
C/Date: 31-May-1996 Sequence revision 1; May-1996 ktext\_change 09-Jul-2004

A/Cross-references: UNIPROT:Q07367; GB:U16555; NID:9293116; PIR:AA20180.1; PID:9293114  
Cisfamily: prolactin

A/Cross-references: UNIPROT:Q07367; GB:U16555; NID:9293116; PIR:AA20180.1; PID:9293114  
Cisfamily: prolactin

Query Match 80.6% Score 84.5; DB 2; Length 217;  
Best Local Similarity 75.6% Pct. Ident. 15;

Matches 165; Conservative 14; Mismatches 22; Indels 15; Gaps 1;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
181 SLNNTVQLCFKDKMNVETPTLALVQCSVSGCF 217

## RESULT 9

Chorionic gonadotropin precursor (alpha hCG-3) - human  
C/Spectat: Homo sapiens  
C/Date: 30-Jun-1998 Sequence revision 30-Jun-1998 ktext\_change 09-Jul-2004

A/Cross-references: UNIPROT:P01243  
Cisfamily: prolactin

Query Match 80.5% Score 84.5; DB 2; Length 217;  
Best Local Similarity 75.6% Pct. Ident. 15;

Matches 169; Conservative 12; Mismatches 19; Indels 17; Gaps 3;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
179 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 215

## RESULT 10

Chorionic gonadotropin - rhesus macaque  
C/Spectat: Macaca mulatta  
C/Date: 31-May-1996 Sequence revision 1; May-1996 ktext\_change 09-Jul-2004

A/Cross-references: UNIPROT:Q07367; GB:U16555; NID:9293116; PIR:AA20180.1; PID:9293114  
Cisfamily: prolactin

Query Match 80.5% Score 84.5; DB 2; Length 217;  
Best Local Similarity 75.6% Pct. Ident. 15;

Matches 169; Conservative 12; Mismatches 19; Indels 17; Gaps 3;

1 MATGRTSLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF--- 57  
1 MAASSTLILALGCLPMLDGRASPPPTTSLDPAHAKHMLKQALPTGQF 60  
58 -----NPGSLGSSSIPTPSRETEQSNLELILGLGSLSPVQRA 105  
61 YIPKESKILKMPDASPTPSRETEQSNLELILGLGSLSPVQRA 105  
106 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 120  
121 SYPNALVQASNSVYDLDLDEBQITLWMLKESGSPPTQYKQYKSPDINSND 165  
166 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 202  
179 ALLNNGVQLCFKDKMNVETPTLALVQCSVSGCF 215





---













PRIOR APPLICATION NUMBER: US 60/407,527  
 PRIOR FILING DATE: 2002-08-28  
 NUMBER OF SEQ ID NOS: 75  
 SOFTWARE: PatentIn version 3.2

SEQUENCE IDENTIFICATION:  
 SEQ ID NO: 799  
 TYPE: DNA  
 ORGANISM: Homo sapiens

US-10-410-962-47

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Score:
1	1,19-127	799	200	0	92.178
Score Similarity:					92.178
Best Local Similarity:					97.188
Query Match:					1
DB:					1

US-09-856-796b-2 (1-202) x US-10-410-962-47 (1-799)

1 160  
 2 160  
 3 160  
 4 160  
 5 160  
 6 160  
 7 160  
 8 160  
 9 160  
 10 160  
 11 160  
 12 160  
 13 160  
 14 160  
 15 160  
 16 160  
 17 160  
 18 160  
 19 160  
 20 160  
 21 160  
 22 160  
 23 160  
 24 160  
 25 160  
 26 160  
 27 160  
 28 160  
 29 160  
 30 160  
 31 160  
 32 160  
 33 160  
 34 160  
 35 160  
 36 160  
 37 160  
 38 160  
 39 160  
 40 160  
 41 160  
 42 160  
 43 160  
 44 160  
 45 160  
 46 160  
 47 160  
 48 160  
 49 160  
 50 160  
 51 160  
 52 160  
 53 160  
 54 160  
 55 160  
 56 160  
 57 160  
 58 160  
 59 160  
 60 160  
 61 160  
 62 160  
 63 160  
 64 160  
 65 160  
 66 160  
 67 160  
 68 160  
 69 160  
 70 160  
 71 160  
 72 160  
 73 160  
 74 160  
 75 160  
 76 160  
 77 160  
 78 160  
 79 160  
 80 160  
 81 160  
 82 160  
 83 160  
 84 160  
 85 160  
 86 160  
 87 160  
 88 160  
 89 160  
 90 160  
 91 160  
 92 160  
 93 160  
 94 160  
 95 160  
 96 160  
 97 160  
 98 160  
 99 160  
 100 160  
 101 160  
 102 160  
 103 160  
 104 160  
 105 160  
 106 160  
 107 160  
 108 160  
 109 160  
 110 160  
 111 160  
 112 160  
 113 160  
 114 160  
 115 160  
 116 160  
 117 160  
 118 160  
 119 160  
 120 160  
 121 160  
 122 160  
 123 160  
 124 160  
 125 160  
 126 160  
 127 160  
 128 160  
 129 160  
 130 160  
 131 160  
 132 160  
 133 160  
 134 160  
 135 160  
 136 160  
 137 160  
 138 160  
 139 160  
 140 160  
 141 160  
 142 160  
 143 160  
 144 160  
 145 160  
 146 160  
 147 160  
 148 160  
 149 160  
 150 160  
 151 160  
 152 160  
 153 160  
 154 160  
 155 160  
 156 160  
 157 160  
 158 160  
 159 160  
 160 160  
 161 160  
 162 160  
 163 160  
 164 160  
 165 160  
 166 160  
 167 160  
 168 160  
 169 160  
 170 160  
 171 160  
 172 160  
 173 160  
 174 160  
 175 160  
 176 160  
 177 160  
 178 160  
 179 160  
 180 160  
 181 160  
 182 160  
 183 160  
 184 160  
 185 160  
 186 160  
 187 160  
 188 160  
 189 160  
 190 160  
 191 160  
 192 160  
 193 160  
 194 160  
 195 160  
 196 160  
 197 160  
 198 160  
 199 160  
 200 160  
 201 160  
 202 160  
 203 160  
 204 160  
 205 160  
 206 160  
 207 160  
 208 160  
 209 160  
 210 160  
 211 160  
 212 160  
 213 160  
 214 160  
 215 160  
 216 160  
 217 160  
 218 160  
 219 160  
 220 160  
 221 160  
 222 160  
 223 160  
 224 160  
 225 160  
 226 160  
 227 160  
 228 160  
 229 160  
 230 160  
 231 160  
 232 160  
 233 160  
 234 160  
 235 160  
 236 160  
 237 160  
 238 160  
 239 160  
 240 160  
 241 160  
 242 160  
 243 160  
 244 160  
 245 160  
 246 160  
 247 160  
 248 160  
 249 160  
 250 160  
 251 160  
 252 160  
 253 160  
 254 160  
 255 160  
 256 160  
 257 160  
 258 160  
 259 160  
 260 160  
 261 160  
 262 160  
 263 160  
 264 160  
 265 160  
 266 160  
 267 160  
 268 160  
 269 160  
 270 160  
 271 160  
 272 160  
 273 160  
 274 160  
 275 160  
 276 160  
 277 160  
 278 160  
 279 160  
 280 160  
 281 160  
 282 160  
 283 160  
 284 160  
 285 160  
 286 160  
 287 160  
 288 160  
 289 160  
 290 160  
 291 160  
 292 160  
 293 160  
 294 160  
 295 160  
 296 160  
 297 160  
 298 160  
 299 160  
 300 160  
 301 160  
 302 160  
 303 160  
 304 160  
 305 160  
 306 160  
 307 160  
 308 160  
 309 160  
 310 160  
 311 160  
 312 160  
 313 160  
 314 160  
 315 160  
 316 160  
 317 160  
 318 160  
 319 160  
 320 160  
 321 160  
 322 160  
 323 160  
 324 160  
 325 160  
 326 160  
 327 160  
 328 160  
 329 160  
 330 160  
 331 160  
 332 160  
 333 160  
 334 160  
 335 160  
 336 160  
 337 160  
 338 160  
 339 160  
 340 160  
 341 160  
 342 160  
 343 160  
 344 160  
 345 160  
 346 160  
 347 160  
 348 160  
 349 160  
 350 160  
 351 160  
 352 160  
 353 160  
 354 160  
 355 160  
 356 160  
 357 160  
 358 160  
 359 160  
 360 160  
 361 160  
 362 160  
 363 160  
 364 160  
 365 160  
 366 160  
 367 160  
 368 160  
 369 160  
 370 160  
 371 160  
 372 160  
 373 160  
 374 160  
 375 160  
 376 160  
 377 160  
 378 160  
 379 160  
 380 160  
 381 160  
 382 160  
 383 160  
 384 160  
 385 160  
 386 160  
 387 160  
 388 160  
 389 160  
 390 160  
 391 160  
 392 160  
 393 160  
 394 160  
 395 160  
 396 160  
 397 160  
 398 160  
 399 160  
 400 160  
 401 160  
 402 160  
 403 160  
 404 160  
 405 160  
 406 160  
 407 160  
 408 160  
 409 160  
 410 160  
 411 160  
 412 160  
 413 160  
 414 160  
 415 160  
 416 160  
 417 160  
 418 160  
 419 160  
 420 160  
 421 160  
 422 160  
 423 160  
 424 160  
 425 160  
 426 160  
 427 160  
 428 160  
 429 160  
 430 160  
 431 160  
 432 160  
 433 160  
 434 160  
 435 160  
 436 160  
 437 160  
 438 160  
 439 160  
 440 160  
 441 160  
 442 160  
 443 160  
 444 160  
 445 160  
 446 160  
 447 160  
 448 160  
 449 160  
 450 160  
 451 160  
 452 160  
 453 160  
 454 160  
 455 160  
 456 160  
 457 160  
 458 160  
 459 160  
 460 160  
 461 160  
 462 160  
 463 160  
 464 160  
 465 160  
 466 160  
 467 160  
 468 160  
 469 160  
 470 160  
 471 160  
 472 160  
 473 160  
 474 160  
 475 160  
 476 160  
 477 160  
 478 160  
 479 160  
 480 160  
 481 160  
 482 160  
 483 160  
 484 160  
 485 160  
 486 160  
 487 160  
 488 160  
 489 160  
 490 160  
 491 160  
 492 160  
 493 160  
 494 160  
 495 160  
 496 160  
 497 160  
 498 160  
 499 160  
 500 160  
 501 160  
 502 160  
 503 160  
 504 160  
 505 160  
 506 160  
 507 160  
 508 160  
 509 160  
 510 160  
 511 160  
 512 160  
 513 160  
 514 160  
 515 160  
 516 160  
 517 160  
 518 160  
 519 160  
 520 160  
 521 160  
 522 160  
 523 160  
 524 160  
 525 160  
 526 160  
 527 160  
 528 160  
 529 160  
 530 160  
 531 160  
 532 160  
 533 160  
 534 160  
 535 160  
 536 160  
 537 160  
 538 160  
 539 160  
 540 160  
 541 160  
 542 160  
 543 160  
 544 160  
 545 160  
 546 160  
 547 160  
 548 160  
 549 160  
 550 160  
 551 160  
 552 160  
 553 160  
 554 160  
 555 160  
 556 160  
 557 160  
 558 160  
 559 160  
 560 160  
 561 160  
 562 160  
 563 160  
 564 160  
 565 160  
 566 160  
 567 160  
 568 160  
 569 160  
 570 160  
 571 160  
 572 160  
 573 160  
 574 160  
 575 160  
 576 160  
 577 160  
 578 160  
 579 160  
 580 160  
 581 160  
 582 160  
 583 160  
 584 160  
 585 160  
 586 160  
 587 160  
 588 160  
 589 160  
 590 160  
 591 160  
 592 160  
 593 160  
 594 160  
 595 160  
 596 160  
 597 160  
 598 160  
 599 160  
 600 160  
 601 160  
 602 160  
 603 160  
 604 160  
 605 160  
 606 160  
 607 160  
 608 160  
 609 160  
 610 160  
 611 160  
 612 160  
 613 160  
 614 160  
 615 160  
 616 160  
 617 160  
 618 160  
 619 160  
 620 160  
 621 160  
 622 160  
 623 160  
 624 160  
 625 160  
 626 160  
 627 160  
 628 160  
 629 160  
 630 160  
 631 160  
 632 160  
 633 160  
 634 160  
 635 160  
 636 160  
 637 160  
 638 160  
 639 160  
 640 160  
 641 160  
 642 160  
 643 160  
 644 160  
 645 160  
 646 160  
 647 160  
 648 160  
 649 160  
 650 160  
 651 160  
 652 160  
 653 160  
 654 160  
 655 160  
 656 160  
 657 160  
 658 160  
 659 160  
 660 160  
 661 160  
 662 160  
 663 160  
 664 160  
 665 160  
 666 160  
 667 160  
 668 160  
 669 160  
 670 160  
 671 160  
 672 160  
 673 160  
 674 160  
 675 160  
 676 160  
 677 160  
 678 160  
 679 160  
 680 160  
 681 160  
 682 160  
 683 160  
 684 160  
 685 160  
 686 160  
 687 160  
 688 160  
 689 160  
 690 160  
 691 160  
 692 160  
 693 160  
 694 160  
 695 160  
 696 160  
 697 160  
 698 160  
 699 160  
 700 160  
 701 160  
 702 160  
 703 160  
 704 160  
 705 160  
 706 160  
 707 160  
 708 160  
 709 160  
 710 160  
 711 160  
 712 160  
 713 160  
 714 160  
 715 160  
 716 160  
 717 160  
 718 160  
 719 160  
 720 160  
 721 160  
 722 160  
 723 160  
 724 160  
 725 160  
 726 160  
 727 160  
 728 160  
 729 160  
 730 160  
 731 160  
 732 160  
 733 160  
 734 160  
 735 160  
 736 160  
 737 160  
 738 160  
 739 160  
 740 160  
 741 160  
 742 160  
 743 160  
 744 160  
 745 160  
 746 160  
 747 160  
 748 160  
 749 160  
 750 160  
 751 160  
 752 160  
 753 160  
 754 160  
 755 160  
 756 160  
 757 160  
 758 160  
 759 160  
 760 160  
 761 160  
 762 160  
 763 160  
 764 160  
 765 160  
 766 160  
 767 160  
 768 160  
 769 160  
 770 160  
 771 160  
 772 160  
 773 160  
 774 160  
 775 160  
 776 160  
 777 160  
 778 160  
 779 160  
 780 160  
 781 160  
 782 160  
 783 160  
 784 160  
 785 160  
 786 160  
 787 160  
 788 160  
 789 160  
 790 160  
 791 160  
 792 160  
 793 160  
 794 160  
 795 160  
 796 160  
 797 160  
 798 160  
 799 160  
 800 160  
 801 160  
 802 160  
 803 160  
 804 160  
 805 160  
 806 160  
 807 160  
 808 160  
 809 160  
 810 160  
 811 160  
 812 160  
 813 160  
 814 160  
 815 160  
 816 160  
 817 160  
 818 160  
 819 160  
 820 160  
 821 160  
 822 160  
 823 160  
 824 160  
 825 160  
 826 160  
 827 160  
 828 160  
 829 160  
 830 160  
 831 160  
 832 160  
 833 160  
 834 160  
 835 160  
 836 160  
 837 160  
 838 160  
 839 160  
 840 160  
 841 160  
 842 160  
 843 160  
 844 160  
 845 160  
 846 160  
 847 160  
 848 160  
 849 160  
 850 160  
 851 160  
 852 160  
 853 160  
 854 160  
 855 160  
 856 160  
 857 160  
 858 160  
 859 160  
 860 160  
 861 160  
 862 160  
 863 160  
 864 160  
 865 160  
 866 160  
 867 160  
 868 160  
 869 160  
 870 160  
 871 160  
 872 160  
 873 160  
 874 160  
 875 160  
 876 160  
 877 160  
 878 160  
 879 160  
 880 160  
 881 160  
 882 160  
 883 160  
 884 160  
 885 160  
 886 160  
 887 160  
 888 160  
 889 160  
 890 160  
 891 160  
 892 160  
 893 160  
 894 160  
 895 160  
 896 160  
 897 160  
 898 160  
 899 160  
 900 160  
 901 160  
 902 160  
 903 160  
 904 160  
 905 160  
 906 160  
 907 160  
 908 160  
 909 160  
 910 160  
 911 160  
 912 160  
 913 160  
 914 160  
 915 160  
 916 160  
 917 160  
 918 160  
 919 160  
 920 160  
 921 160  
 922 160  
 923 160  
 924 160  
 925 160  
 926 160  
 927 160  
 928 160  
 929 160  
 930 160  
 931 160  
 932 160  
 933 160  
 934 160  
 935 160  
 936 160  
 937 160  
 938 160  
 939 160  
 940 160  
 941 160  
 942 160  
 943 160  
 944 160  
 945 160  
 946 160  
 947 160  
 948 160  
 949 160  
 950 160  
 951 160  
 952 160  
 953 160  
 954 160  
 955 160  
 956 160  
 957 160  
 958 160  
 959 160  
 960 160  
 961 160  
 962 160  
 963 160  
 964 160  
 965 160  
 966 160  
 967 160  
 968 160  
 969 160  
 970 160  
 9









УВ-09-856-796b-2.гпрб

[illegible]

Search completed: February 7, 2005, 17:06:43  
Job time : 339 secs

Copyright (c) 1993 - 2005 Compaq Inc.

On protein - nucleic search, using time.plane model

Run on: February 7, 2005, 13:31:06, Search time 180 Seconds

1856.266 Million cell updates/sec

Title: US-09-856-796D-2

Sequence: 1 MYGSRSTLLALAGLCPW.....XVFPLALGSRVDSQCR 202

Scoring table:

BLASTN2

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Gapop 6.0, Gapext 7.0

Gapex 6.0, Dextx 7.0

Searched: 120784 seqs, 8181395 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 08

Maximum March 1008

Listing filter: 45 duplicates

Command line parameters:

Model: time.plane.model, -DEV-V21b

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

Database: /usr/local/ncbi/blast/blastdb

00 DEC-70 68-2 (1-202) X 118-09-284-878-2 (1-663)

[illegible]

```

      1
      2
      3
      4
      5
      6
      7
      8
      9
     10
     11
     12
     13
     14
     15
     16
     17
     18
     19
     20
     21
     22
     23
     24
     25
     26
     27
     28
     29
     30
     31
     32
     33
     34
     35
     36
     37
     38
     39
     40
     41
     42
     43
     44
     45
     46
     47
     48
     49
     50
     51
     52
     53
     54
     55
     56
     57
     58
     59
     60
     61
     62
     63
     64
     65
     66
     67
     68
     69
     70
     71
     72
     73
     74
     75
     76
     77
     78
     79
     80
     81
     82
     83
     84
     85
     86
     87
     88
     89
     90
     91
     92
     93
     94
     95
     96
     97
     98
     99
    100
    101
    102
    103
    104
    105
    106
    107
    108
    109
    110
    111
    112
    113
    114
    115
    116
    117
    118
    119
    120
    121
    122
    123
    124
    125
    126
    127
    128
    129
    130
    131
    132
    133
    134
    135
    136
    137
    138
    139
    140
    141
    142
    143
    144
    145
    146
    147
    148
    149
    150
    151
    152
    153
    154
    155
    156
    157
    158
    159
    160
    161
    162
    163
    164
    165
    166
    167
    168
    169
    170
    171
    172
    173
    174
    175
    176
    177
    178
    179
    180
    181
    182
    183
    184
    185
    186
    187
    188
    189
    190
    191
    192
    193
    194
    195
    196
    197
    198
    199
    200
    201
    202
    203
    204
    205
    206
    207
    208
    209
    210
    211
    212
    213
    214
    215
    216
    217
    218
    219
    220
    221
    222
    223
    224
    225
    226
    227
    228
    229
    230
    231
    232
    233
    234
    235
    236
    237
    238
    239
    240
    241
    242
    243
    244
    245
    246
    247
    248
    249
    250
    251
    252
    253
    254
    255
    256
    257
    258
    259
    260
    261
    262
    263
    264
    265
    266
    267
    268
    269
    270
    271
    272
    273
    274
    275
    276
    277
    278
    279
    280
    281
    282
    283
    284
    285
    286
    287
    288
    289
    290
    291
    292
    293
    294
    295
    296
    297
    298
    299
    300
    301
    302
    303
    304
    305
    306
    307
    308
    309
    310
    311
    312
    313
    314
    315
    316
    317
    318
    319
    320
    321
    322
    323
    324
    325
    326
    327
    328
    329
    330
    331
    332
    333
    334
    335
    336
    337
    338
    339
    340
    341
    342
    343
    344
    345
    346
    347
    348
    349
    350
    351
    352
    353
    354
    355
    356
    357
    358
    359
    360
    361
    362
    363
    364
    365
    366
    367
    368
    369
    370
    371
    372
    373
    374
    375
    376
    377
    378
    379
    380
    381
    382
    383
    384
    385
    386
    387
    388
    389
    390
    391
    392
    393
    394
    395
    396
    397
    398
    399
    400
    401
    402
    403
    404
    405
    406
    407
    408
    409
    410
    411
    412
    413
    414
    415
    416
    417
    418
    419
    420
    421
    422
    423
    424
    425
    426
    427
    428
    429
    430
    431
    432
    433
    434
    435
    436
    437
    438
    439
    440
    441
    442
    443
    444
    445
    446
    447
    448
    449
    450
    451
    452
    453
    454
    455
    456
    457
    458
    459
    460
    461
    462
    463
    464
    465
    466
    467
    468
    469
    470
    471
    472
    473
    474
    475
    476
    477
    478
    479
    480
    481
    482
    483
    484
    485
    486
    487
    488
    489
    490
    491
    492
    493
    494
    495
    496
    497
    498
    499
    500
    501
    502
    503
    504
    505
    506
    507
    508
    509
    510
    511
    512
    513
    514
    515
    516
    517
    518
    519
    520
    521
    522
    523
    524
    525
    526
    527
    528
    529
    530
    531
    532
    533
    534
    535
    536
    537
    538
    539
    540
    541
    542
    543
    544
    545
    546
    547
    548
    549
    550
    551
    552
    553
    554
    555
    556
    557
    558
    559
    560
    561
    562
    563
    564
    565
    566
    567
    568
    569
    570
    571
    572
    573
    574
    575
    576
    577
    578
    579
    580
    581
    582
    583
    584
    585
    586
    587
    588
    589
    590
    591
    592
    593
    594
    595
    596
    597
    598
    599
    600
    601
    602
    603
    604
    605
    606
    607
    608
    609
    610
    611
    612
    613
    614
    615
    616
    617
    618
    619
    620
    621
    622
    623
    624
    625
    626
    627
    628
    629
    630
    631
    632
    633
    634
    635
    636
    637
    638
    639
    640
    641
    642
    643
    644
    645
    646
    647
    648
    649
    650
    651
    652
    653
    654
    655
    656
    657
    658
    659
    660
    661
    662
    663
    664
    665
    666
    667
    668
    669
    670
    671
    672
    673
    674
    675
    676
    677
    678
    679
    680
    681
    682
    683
    684
    685
    686
    687
    688
    689
    690
    691
    692
    693
    694
    695
    696
    697
    698
    699
    700
   
```



[illegible]



1	SOFTWARE: FASTEST FOR Windows Version 4.0	
1	SEO ID NO 2789	
1	LENGTH: 1132	
1	TYPE: DNA	
1	ORGANISM: human	
1	US-09-949-016-2789	
Alignment Scores:		
	1.25e+09	Length: 1132

Percent Similarity:	66.56%	Conserved:	66.56%
Percent Identity:	66.56%	Mismatches:	66.56%

DB: 4 GAPB:

US-09-856-Z (A-Z) X 0000

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

21 LeuGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer

Dd  
177 CTTCAAGAGGGCAGTGCCTCCGAAACAIATCCATTACCGGCG.....

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

-----AsnProGlnThrSerLeuCysPhe

D<sub>b</sub> 297 TATATCCAAAGGACAGAGTATTCAITTCCTGCAGAACCCCAGACCCCCA.....

[illegible]

ac : aut aut tle sort au le u e u i e g l n s e r t r p l e u c l u p r o v a l g l n p h e u a r

Db  
417 CTGCTCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAATTCCCTCAAG

06 ServAlphenlaabserledvallylglyndaserwpcalindn

22 ..... 22

537 AAGGACCTAGAGGAGGCATCCAAACGCTGATGGGGTGAGGGTGCCGCCAGGAGTCC

QY 137 -----

D5 59 / MAILING INFORMATION

5'-GAGGAACTCACCCTATTCCTCATTTCCCGTGAATCCT

237 -----

[illegible][illegible]

141 MGIVSERPROARGTHRGYGINILEPHELYGLNTHRTYRSERYEPHEASPTHRANS

Db 837 TGGCAGCCCCCGGACTGGGCAATCTTCAAGCAGACCTACAGCAGGTTGGGACAGGAGG

[illegible]







161 FHLA...  
 897 AGCA...  
 181 FHLA...  
 957 GCA...  
 201 YPHE 202  
 1017 CTTG 1020  
 RESULT 13  
 US-09-856-796b-2  
 Patent No. 6812339  
 GENERAL INFORMATION: J. Craig et al.  
 TITLE OF INVENTION: WITH PROBABILISTIC METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C100107  
 CURRENT APPLICATION NUMBER: US/09/949 016  
 PRIOR APPLICATION NUMBER: 06-01-14  
 PRIOR FILING DATE: 2000-10-20/24.1.755  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-09-06/23.1.498  
 PRIOR APPLICATION NUMBER: 2000-09-06/23.1.498  
 SOFWARE: SEQ ID NO: 207012  
 SEQ ID NO 2793  
 LENGTH: 1132  
 ORGANISM: Human  
 US-09-856-796b-2 (1-202) x US-09-949-016-2793 (1-1132)  
 Alignment Scores:  
 Pred. No. 1,356-109 Length: 1132  
 Score: 959.50  
 Percent Similarity: 66.56  
 Query Similarity: 66.56  
 Query Match: 4  
 Mismatches: 0  
 Gaps: 2  
 1 MEAL...  
 117 AGCA...  
 21 LAG...  
 177 GCA...  
 41 LAG...  
 237 CCA...  
 58 -----  
 297 TAT...  
 66 SGA...  
 357 TCA...  
 86 LAG...  
 417 CCA...  
 106 SGA...  
 477 AGCA...  
 126 YPHE...  
 537 AGCA...  
 137 AGCA...  
 597 AGCA...  
 137 AGCA...  
 657 AGCA...  
 717 CCA...  
 138 -----  
 777 GCA...  
 141 PLY...  
 837 TGA...  
 161 FHLA...  
 897 AGCA...  
 181 FHLA...  
 957 GCA...  
 201 YPHE 202  
 1017 CTTG 1020  
 RESULT 14  
 US-09-187-756c-1  
 Sequence 1, Application US/08187756C  
 Patent No. 5597709  
 APPLICANT: ROSEN, ET AL.  
 TITLE OF INVENTION: Human Growth Hormone  
 NUMBER OF SEQUENCES: 7  
 ADDRESS: BAYER, BAY, GILFILLAN,  
 ADDRESS: CROCI, STEWART & GILFILLAN,  
 STREET: 6 BECKER PARK ROAD  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 CITY: 07068  
 COMPTON, NEW JERSEY  
 MEDIUM TITRABLE FORM  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 CURRENT APPLICATION NUMBER: 5.1  
 FILING DATE: January 27, 1994  
 PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER:  
 FILING DATE: INFORMATION:  
 NAME: FERARO, GREGG  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 32800-55  
 TELEPHONE: 201-594-1100



us-09-856-796b-2.rn1

Page 11

Search completed: February 7, 2005, 15:53:21  
Job time : 188 secs

***This Page Blank (uspto)***

















[illegible]

## Qy

DB

QY

부

2

QY

DB

QY

DB

or

2

8

QY

D5

## RESULTS

ADRES  
ID

XX  
AC

XXII

XX

DE  
XX

22

ECN

XIX

xx 90

FH  
ET

PT

XX FT

PN  
XX

PD

• **XY**



**Table 1**

Variable	Mean	SD	Range
Age (years)	67.8	9.0	45-85
Gender (% male)	75.0	-	-
Marital status (% married)	75.0	-	-
Educational level (% college graduate)	75.0	-	-
Income (\$1000/monthly)	1.8	0.8	0-4
Health status (% good)	75.0	-	-
Exercise frequency (% weekly)	75.0	-	-
Social support (% strong)	75.0	-	-
Stress level (% low)	75.0	-	-
Mental health (% good)	75.0	-	-
Physical health (% good)	75.0	-	-
Quality of life (% good)	75.0	-	-

41 LeuArgAlaHisArgGluHisGlnLeuAlaPheAspThrTyrgLnsIuphe-

5









***This Page Blank (uspio)***



Page 2

REFERENCE  
AUTHORS  
JOURNAL  
1  
Haefliger, A. and Hirsch, F.  
Patent: FR 2786194-A 1 26-MAY-2000,  
CENTRE NAT RECH SCIENT (FR)

CDS

```

CM8      1--609
         /note="unnamed protein product"
         /codon_usage=1
         /protein_id="CA09004.1"
         /db_xref="GI:10187117"
         /translation="MTQSTGSLAAAGCLCTIPMLQSGSAPPTPLSLR,PMDASGLAA
         RLQGLAPVYQGFNPQTSLSCEHSIPLRNNEHQKQSNLRLRLSILLQSHLEPVV

```

607

SECRET

Pred. No.:	1.3e-103	Length:	202
Score:	1047.00	Matches:	202

Percent Similarity:	100.00%	Conserved:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match:	100.00%	0
DB:	6	
Gaps:		

US-09-856-796B-2 (1-202) X AX025440 (1-609)

1 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheCysLeuAlaCysLeuProIleAsp

[illegible][illegible]

**61** CTTCAGAGGCGCAGTCCCTCCCAACCAAATCCCATTACCCTGG.....  
pb

41 Lewatgahilwagilehnbomobowalehnoyehayey  
oy

[illegible]

01 ATTGCTGGCCGCAACCGAGGATGAGTGGAAACACACACAG 2

[illegible]

261 | AATTCGACCGAGACTGCTCCGATCTCCCTGCTCATTCACAGTGTGGCTGAGGCC 3

101 ValGlnPheLeuAArgSerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 1

301 GTGCACTTCCTCAGGAGTGTCTTCCGCAACAGCCCTGTGTACGGCGCCCTTGACACGAC 3

121 ValTyrAspLeuLeuLysAspLeuGluGluYrIleGlnThrLeuMetGlyArgLeuGluI

Db 361 GTCTATGACCTCTAAAGACCTAGAGGAGGCTCCAAACGCTGA TGGGAGGGCTGGAA

141 ArgGlySerProArgThrGlyGlnIlePheIleGlnThrTyrSerIysPheAspThrAsn

Db 421 GATGACACCCCCCGACTGGGCGATCTTCAGGACACCTACAGCGAGTTGACACACAC

161 SerHisAsnArgProAlaLeuLeuLeuValSerTyrGlyLeuLeuLysIcysPheValGluGln

D8 TCACAGGATGCTACTCAGGATTACGGTCCCTTCCTTTCTGTGC

101 Metaphys Valsignani, *Il verbo e il verbo* (1971), pp. 111-112.

**Dd**

541 ATGGACAGGCGTCGATGCATTCTTCCCAACTCACCCTTTTGCTGTG  
.....

QY  
201 Glycerol 202  

000 311-7000 Y09









FEATURES	source
OS	Artificial gene; Genes.
PN	JP 198620689-A/1
PD	JP 85-1385 JP 1985042404
PT	WAKUJIMA KENJO, NAGAI YUN
PC	CLIN5/00//C12P1/02/
CC	strandedness: double;
CC	topology: linear;
CC	topology: alt: No;
CC	int1: sense: No;
PH	Location/Qualifiers
Key	
PH	280
FT	misc:feature
FT	/note="G(3)n"
FT	1107
FT	misc:feature
FT	/note="A(n)n".
FT	Location/Qualifiers
1.	.3417
/segment="synthetic construct"	
/segment="genomic DNA"	
/db:ref="taxon:32630"	

[illegible]

RESULTS	9	654 bp	DNA	linear	PAT 16-AUG-200
AC131369					
LOCUS	AK881369.3	3 from RefSeq	MO2055532.		
DEFINITION	AK881369.3				
ACCESSION	AK881369				
VERSION	AK881369.1	GI:2213686			
KEYWORDS					
SOURCE					
ORGANISM	Canis familiaris (human)				
	Brain; spleen				
	Myxoid sarcoma				
	Rhalyote; Mesozoa; Chordata; Canidae; Canis lupus familiaris (domestic dog);				
	Mammalia; Euteuthera; Primates; Chelonia; Testudines; Homo.				
REFERENCES					
	Anderson, K.V., Druetman, J., and Christensen, J.				
	Improved growth hormone molecular				
	patent: WO 02/05532. Myxogen Holdings Ltd. (x)				
TITLE					
JOURNAL					
	Myxogen				
FEATURES					
	Location/Qualifiers				
source	1..654				









Tue Feb 8 14:23:53 2005

us-09-856-796b-2.rge

Page 11

[illegible]

Search completed: February 7, 2005, 14:57:15  
Job time : 4149 secs

***This Page Blank (uspto)***



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using pw model

Run on:

February 6, 2005, 13:04:34 : Search time 322 seconds

48,940 alignments  
48,940 million cell updates/sec

Title: US-09-856-796b-2

Sequence score: 1047

1 MATSRSTLLATGCLPMQ.....KMTFRTATGCSYSGSGCF 202

Scoring table:

Gapop 10.0 , Gapeat 0.5

Searched: 137511 seqs, 335702437 residues

Total number of hits satisfying chosen parameters: 137511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing files 45 summaries

Database:

No.	Score	Match length	DB ID	Description
1	1029.5	98.3	217	US-09-853-688-2
2	1029.5	98.3	217	US-09-853-688-4
3	1029.5	98.3	217	US-09-969-748-C
4	1029.5	98.3	217	US-10-788-318-2
5	1029.5	98.3	217	US-10-788-318-4
6	1024.5	97.9	217	US-09-923-819-6
7	1024.5	97.9	217	US-09-804-609-16
8	1017.5	97.2	217	US-10-411-037-48
9	1017.5	97.2	217	US-10-411-037-48
10	1017.5	97.2	217	US-10-411-037-48
11	1017.5	97.2	217	US-10-411-037-48
12	1017.5	97.2	217	US-10-411-037-48
13	1017.5	97.2	217	US-10-411-037-48
14	1017.5	97.2	217	US-10-411-037-48
15	1017.5	97.2	217	US-10-411-037-48
16	1017.5	97.2	217	US-10-411-037-48
17	1017.5	97.2	217	US-10-411-037-48
18	1017.5	97.2	217	US-10-411-037-48
19	1017.5	97.2	217	US-10-411-037-48
20	1017.5	97.2	217	US-10-411-037-48

Ped. No. is the number of results provided by chance to have a score greater than or equal to the best result being printed, and is derived by analysis of the total score distribution.

#### SIMILARITIES

Query Match	Score	Match length	DB ID	Description
1	1029.5	98.3	217	US-09-853-688-2
2	1029.5	98.3	217	US-09-853-688-4
3	1029.5	98.3	217	US-09-969-748-C
4	1029.5	98.3	217	US-10-788-318-2
5	1029.5	98.3	217	US-10-788-318-4
6	1024.5	97.9	217	US-09-923-819-6
7	1024.5	97.9	217	US-09-804-609-16
8	1017.5	97.2	217	US-10-411-037-48
9	1017.5	97.2	217	US-10-411-037-48
10	1017.5	97.2	217	US-10-411-037-48
11	1017.5	97.2	217	US-10-411-037-48
12	1017.5	97.2	217	US-10-411-037-48
13	1017.5	97.2	217	US-10-411-037-48
14	1017.5	97.2	217	US-10-411-037-48
15	1017.5	97.2	217	US-10-411-037-48
16	1017.5	97.2	217	US-10-411-037-48
17	1017.5	97.2	217	US-10-411-037-48
18	1017.5	97.2	217	US-10-411-037-48
19	1017.5	97.2	217	US-10-411-037-48
20	1017.5	97.2	217	US-10-411-037-48

#### ALIGNMENTS

Query Match	Score	Match length	DB ID	Description
1	1029.5	98.3	217	US-09-853-688-2
2	1029.5	98.3	217	US-09-853-688-4
3	1029.5	98.3	217	US-09-969-748-C
4	1029.5	98.3	217	US-10-788-318-2
5	1029.5	98.3	217	US-10-788-318-4
6	1024.5	97.9	217	US-09-923-819-6
7	1024.5	97.9	217	US-09-804-609-16
8	1017.5	97.2	217	US-10-411-037-48
9	1017.5	97.2	217	US-10-411-037-48
10	1017.5	97.2	217	US-10-411-037-48
11	1017.5	97.2	217	US-10-411-037-48
12	1017.5	97.2	217	US-10-411-037-48
13	1017.5	97.2	217	US-10-411-037-48
14	1017.5	97.2	217	US-10-411-037-48
15	1017.5	97.2	217	US-10-411-037-48
16	1017.5	97.2	217	US-10-411-037-48
17	1017.5	97.2	217	US-10-411-037-48
18	1017.5	97.2	217	US-10-411-037-48
19	1017.5	97.2	217	US-10-411-037-48
20	1017.5	97.2	217	US-10-411-037-48

us-09-856-796b-2.rapb

```

; PRIOR APPLICATION NUMBER: US 60/237, 929
;
; PRIOR FILING DATE: 2000-10-02
;
; NUMBER OF SEQ ID NOS: 115
;
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 4
;
; LENGTH: 217
;
; name: none

```

Query Match	98.3%	Score 1029.5;	DB 10;	Length 217
Best Local Similarity	93.1%	Pred. No. 1.1e-93;		
Matches 203;	Conservative	0;	Mismatches	0;
			Indels	15;

1 MATGRTSLTAPGLCTPWIQGSAFPTPLSRLEFNASLRARRHQLAPDTYQEF--- 51

58 -----NPTSLCPSEBIPTPSNRETOCKSNLELRISLLLIQSMLEPVQPLR 105

61 YIPKQKYSFLQNPQTSLSCESESIFTPSNKEETQKSNLBRLISLLIQSWLEPVQFLR 120

QY 106 SVFANSLVYGASDSNVYLDKLBLEGIQTLMGRLEBOSPRGCGIFKQYTSKFEDTNSHND 165  
|||||  
|||||

Db 122 SVFASLSLVYCASDSNNYDLKKDLRRGLQILMKRKBDSGKRCQGRVAV-----  
Cc 166 ALIKRYGLVCFRKMDKVFTEFLRIYQCRSVSGSGCF 202

181 ALKRYGLYCFRQNDKVFTRIVQCRSVESGCF 217

RESULT 4  
10.708-310.3

```
US-10-100-210 2
! Sequence 2, Application US/10780318
! Publication No. US2004037510A1
! UNPROCESSED.
```

GENERAL INFORMATION: DAVID N.  
APPLICANT: COOPER,  
APPLICANT: PROCTOR, ANNIE M.  
PROCESSED: TONIN

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

```

; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: patentIn Ver. 2.1

```

```

      SEQ ID NO 2
      /
      LENGTH: 217
      TYPE: prt

```

ORGANISM: Homo sapiens  
US-10-788-318-2

Query Match	98.3%	Score 1029.5	DB16	Length 217
Best Local Similarity	93.1%	Pred. 1.1e-93		
Best Overall Similarity	93.1%			
Mismatches	0	Indels	0	Gaps

Matches	2021	Current	Next
1	MATSRSTIIAFGLCLPWIOGSAFPTPLSRLEFNASIRAHRLHQLAFPTYOOF---	57	

1 MATGKRTSLILAFGLLCTFMIDGGSAFTIPISRLDNASLRHRLHQLAFTDYQSEEA 60

QY 58 -----NPTSLCSFSSSIFITFSAKELVQ  
Db 61 YIPKQKYSFLANPQTSICFSSSIFITFSNRSESTQCKENMLTELRLSLTLTIQSWLEPVPQFLR 12

QY 106 SVEANSI.VYGAJSDSN.VYDOLKXLEBGIOTIMGRLEJDS.PRTGOI FKOTYSKFTJNSHND 1 6

Db 121 SYFANSLVYGGADSDNVYDLLKDLKEEGIQTLMLGRLKDSFRIVQAFNVLINR<sup>22</sup>ENRHRN<sup>23</sup>

181 ALAKNYGLLYCFRKDMKVEYETLRIVQCRSEVSGSGF 217





Tue Feb 8 14:23:52 2005

us-09-856-796b-2.rapb

Page 5

Qy MATGSTRILLATVGLLPLMLQKSA PPTLPLRLRNALSLAHLHQA PTTQFQ -- 57  
Qy 1 MATGSTRILLATVGLLPLMLQKSA PPTLPLRLRNALSLAHLHQA PTTQFQ -- 57  
Qy 58 --NPGRSLGASSTLPPTPRPSPKQSNLRLRLSLGSLGSLPFLR 60  
Db 61 YIPKQKSTFQNLQVSLGSSSTLPPTPRSPKQSNLRLRLSLGSLGSLPFLR 12  
Qy 126 SPVAPSLVYGASSTVYGLLQKLRLSGQ LKMLAHLRQSGNQLPQPTPRKPTNSND 16  
Qy 126 SPVAPSLVYGASSTVYGLLQKLRLSGQ LKMLAHLRQSGNQLPQPTPRKPTNSND 16  
Qy 161 ALKRVSLVYQASSTVYGLLQKLRLSGQ LKMLAHLRQSGNQLPQPTPRKPTNSND 184  
Db 166 ALKRVSLVYQASSTVYGLLQKLRLSGQ LKMLAHLRQSGNQLPQPTPRKPTNSND 184  
Qy 181 ALKRVSLVYQASSTVYGLLQKLRLSGQ LKMLAHLRQSGNQLPQPTPRKPTNSND 217

[illegible]

Db 181 ALFQNYGLLYCFRKMDKVELRIVQCRSVEGSGCF 217

```

RESULT 13
Qy Sequence 48: US09046101516M1
GENERAL INFORMATION:
APPLICANT: Niose Technology, Inc.
INVENTOR: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Baker, Robert
APPLICANT: Baker, David
APPLICANT: Baker, David
APPLICANT: Bove, Caryn
TITLE OF INVENTION: INTERFERON BETA; REMODELING AND GLYCOCONJUGATION OF INTERFERON BETA
FILE OF INVENTION: BETA
CURRENT APPLICATION NUMBER: 09046101516
PRIORITY DATE: 2003-04-09
PRIORITY FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,652
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,992
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/391,774
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/356,594
PRIOR FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/407,527
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SD NO: 48
SD NAME: 1
SD TYPE: PAT
ORGANISM: Homo sapiens
Query Match 97.2%; Score 1017.5; DB: Length 217;
Beat Local Similarity 92.2%; Pmed No: 0;
Matches 200; Conservative Q; Mismatches 2; Indels 15; Gaps 1;
Oy 1 MAGSTSTLLAELCLGCMCGGGATPTTSLSEFLNLSLRHGLAPVYEE-- 57
1 MAGSTSTLLAELCLGCMCGGGATPTTSLSEFLNLSLRHGLAPVYEE-- 57
Db 1 MAGSTSTLLAELCLGCMCGGGATPTTSLSEFLNLSLRHGLAPVYEE-- 57
Oy 58 -----WQSCTCSSTSPNNRETRDONSLELISILLIWSLEVPFIR 105
-----WQSCTCSSTSPNNRETRDONSLELISILLIWSLEVPFIR 105
Db 61 YIMEKSYFPDPSTSCRESPIPSNEETVDNLISILLIWSLEVPFIR 105
YIMEKSYFPDPSTSCRESPIPSNEETVDNLISILLIWSLEVPFIR 105
Oy 106 SPYNALTVGSNSNYWLYLVNMGQTGMENLSENPFTQIPQTSYFFTPSHND 120
SPYNALTVGSNSNYWLYLVNMGQTGMENLSENPFTQIPQTSYFFTPSHND 120
Db 121 SYGNALTVGSNSNYWLYLVNMGQTGMENLSENPFTQIPQTSYFFTPSHND 165
SYGNALTVGSNSNYWLYLVNMGQTGMENLSENPFTQIPQTSYFFTPSHND 165
Oy 166 ALLNGVGLTYFKMDKDYVFPAIVGVSSGSGV 202
ALLNGVGLTYFKMDKDYVFPAIVGVSSGSGV 202
Db 181 ALLNGVGLTYFKMDKDYVFPAIVGVSSGSGV 217
ALLNGVGLTYFKMDKDYVFPAIVGVSSGSGV 217
RESULT 13
US0410-997-48
Sequence 48: US10410997
GENERAL INFORMATION:
APPLICANT: Niose Technology, Inc.
INVENTOR: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Baker, Robert
APPLICANT: Baker, David
APPLICANT: Baker, David
APPLICANT: Bove, Caryn
TITLE OF INVENTION: INTERFERON BETA; REMODELING AND GLYCOCONJUGATION OF INTERFERON BETA
FILE OF INVENTION: BETA
CURRENT APPLICATION NUMBER: 09046101516
PRIORITY DATE: 2003-04-09
PRIORITY FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,652
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,992
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/391,774
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/356,594
PRIOR FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/407,527
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SD NO: 48
SD NAME: 1
SD TYPE: PAT
ORGANISM: Homo sapiens

```

us-09-856-796b-2.rapd

```

APPLICANT: Hakes, David
APPLICANT: Bove, Carolyn
TITLE OF INVENTION: REMODELING AND GLYCOSYLATION OF
TITLE OF INVENTION: FSH
FILE REFERENCE: 040851-01-5059
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR PILING DATE: 2001-10-10/60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2001-10-10/60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PILING DATE: 2002-06-07/60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-07-17/60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PILING DATE: 2002-07-17/60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-28/60/417,527
PRIOR APPLICATION NUMBER: US 60/417,527
NUMBER OF SEQ ID NOS: 75
SEQ ID NO: 1
SOFTWARE: Preclen version 3.2
SEQUENCE LENGTH: 217
TYPE: PRT
ORGANISM: Homo sapiens
Query Match      97.2% Score 1017.5 DB 16, Length 217;
Best Local Statistcally 72.2% 0; Mismatches 2, Indels 15, Gaps 1,
Matches 200; Conservative
Dy Db Oy Qy Dy Db Oy Qy Dy Db Oy Qy Dy Db Oy Qy Dy Db Oy Qy Dy Db Oy Qy
1 MATGTFSLILALPGLICLWQDSFPTIPARLPKLEPNRDLAKHQLADTGVF--- 57
1 NALSSTFSLILALPGLICLWQDSFPTIPARLPKLEPNRDLAKHQLADTGVF 60
58 -----NVTSLTPSERSPIPRNERTVQSNNGLRLSGILLIQQWLSPYQVLA 105
61 YIRKSNISLVGNASIDNVYDLDELRIQTLMQRLEDSSPTQITRGTSRRHQND 120
106 SVANSISLVGNASIDNVYDLDELRIQTLMQRLEDSSPTQITRGTSRRHQND 165
121 SVANSISLVGNASIDNVYDLDELRIQTLMQRLEDSSPTQITRGTSRRHQND 180
166 ALTNVYGLLCYTRSDMDKRYETPLATVGSNSGSCGR 202
181 ALTNVYGLLCYTRSDMDKRYETPLATVGSNSGSCGR 217
RESULT 14
US-10-411-012-48
Sequence 6; Application US1041012
Accession No.US200401366021
GENERAL INFORMATION:
APPLICANT: Nocris Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Bove, Carolyn
TITLE OF INVENTION: GLYCOSYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHUSEIN
FILE REFERENCES: 53
CURRENT PILING DATE: 2003-04-09/60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PILING DATE: 2003-04-09/60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2003-04-09/60/387,292
PRIOR APPLICATION NUMBER: US 60/387,292

```

PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-08  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-06  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Preclint version 3.2  
SEQ ID NO: 48  
SEQ ID NO: 49  
ORGANISM: Homo sapiens  
TYER: PRT  
US-10-411-02-48

Query Match  
Best Local Similarity 92.2%; Pred. Misclassification 57  
Matches 200; Conservative 0; Miscellaneous 2; Indels 15; Gaps 1

Dy 1 MANGSRRLILLFQDLICWVAGSGGAPPLPILSLPTNLSLAWYNGCLAPDTGGF---  
Db 1 MARGSRRLILLFQDLICWVAGSGGAPPLPILSLPTNLSLAWYNGCLAPDTGGF 60  
Dy -----S-----  
Db -----S-----  
Dy 58 -----NQGISCSPEEIPYSNRFTQSNLELLRNLIRITLIGTSPVQTE 105  
Db 61 VIKEDNSFLAKDYTCISSEIPISSHALLQNSLELLRNLIRITLIGTSPVQTE 105  
Dy 106 SVANSIVYGNDGVNYLLKQDEGTQLMRLENPSPTQTQVLRSGPNRGND 150  
Db 106 SVANSIVYGNDGVNYLLKQDEGTQLMRLENPSPTQTQVLRSGPNRGND 150  
Dy 121 SVANSIVYGNDGVNYLLKQDEGTQLMRLENPSPTQTQVLRSGPNRGND 180  
Db 121 SVANSIVYGNDGVNYLLKQDEGTQLMRLENPSPTQTQVLRSGPNRGND 180  
Dy 166 ALTKAVGLLYCPENDGVNYLVETATLVGCSVSSTGCF 202  
Db 166 ALTKAVGLLYCPENDGVNYLVETATLVGCSVSSTGCF 202  
Dy 181 ALTKAVGLLYCPENDGVNYLVETATLVGCSVSSTGCF 217  
Db 181 ALTKAVGLLYCPENDGVNYLVETATLVGCSVSSTGCF 217

RESULT 15  
US-10-287-994-48  
Sequence 48: US10287994.US10287994  
Accession No: US00401375511  
GENERAL INFORMATION:  
APPLICANT: Neseo Technologies, Inc.  
INVENTOR: David Robert  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Bower, Carolyn  
APPLICANT: Baker, Xiyid  
TITLE OR INVENTION: REMODELING AND GLYCOCOMMUNICATION OF PEPTIDES  
FILE REFERENCE: 040853-01-5052-00  
CURRENT APPLICATION NO: 040853-01-5052-00  
PRIOR APPLICATION NUMBER: US 60/387,994  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,592  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/387,992  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-08  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-06  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: Patent version 3.1  
SEQ ID NO: 48  
SEQ ID NO: 49  
LENGTH: 217  
TYPE: PRT



*This Page Blank (uspto)*





The Feb 8 14:23:52 2005

Matches 202: Conservative 0, Mismatches 0, Indels 15, Gaps 1,  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 57  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 60  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 63  
 58 -----NPGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 105  
 61 YIPKQVYFYLQNGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 120  
 106 SYPMNSLYVQAGSNVYLLADDEQITMWRDLSDSPRQQLPQGTSAFTTNSND 165  
 121 SYPMNSLYVQAGSNVYLLADDEQITMWRDLSDSPRQQLPQGTSAFTTNSND 180  
 166 ALANNTALTYCFRPMQDQVTFPLAVQCSVSSGCF 202  
 181 ALANNTALTYCFRPMQDQVTFPLAVQCSVSSGCF 217

RESULT 2  
 US-08-459-451  
 Sequence 51: Application US/08469658  
 Patent No. 5917018

GENERAL INFORMATION:  
 INVENTOR: Peter A. Green, Hans Christian  
 APPLICANT: Holtec, Thor Lab  
 APPLICANT: Holtec, Thor Lab  
 TITLE OF INVENTION: METHOD FOR THE RECODING OF  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Peter A. Green, Hans Christian  
 ADDRESS: 1435 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts

COUNTRY: USA  
 ZIP: 02110-3804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Pictent Release #1.0, Version  
 SOFTWARE: #1.25  
 CURRENT APPLICATION NUMBER: US/08/469,658  
 FILING DATE: June 5, 1995

CLASSIFICATION: 530  
 PRIOR APPLICATION NUMBER: 08/199,060  
 FILING DATE: February 4, 1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 06/663/002002  
 TELECOMMUNICATIONS: 617 542 5070  
 TELEFAX: 617 542 8906

TELEX: 200154  
 INFORMATION: 100000 ID NO: 51  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 217 amino acids  
 TYPE: amino acid  
 STRANDS: linear  
 MOLECULE TYPE: protein  
 US-08-469-451

Query Match 98.3% Score 1024.5; DB 2; Length 217;  
 Best Local Similarity 93.1% Pred. No. 1.9e-108;  
 Matches 202: Conservative 0, Mismatches 0, Indels 15, Gaps 1;  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 57

DB  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 60  
 58 -----NPGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 105  
 61 YIPKQVYFYLQNGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 120  
 106 SYPMNSLYVQAGSNVYLLADDEQITMWRDLSDSPRQQLPQGTSAFTTNSND 165  
 121 SYPMNSLYVQAGSNVYLLADDEQITMWRDLSDSPRQQLPQGTSAFTTNSND 180  
 166 ALANNTALTYCFRPMQDQVTFPLAVQCSVSSGCF 202  
 181 ALANNTALTYCFRPMQDQVTFPLAVQCSVSSGCF 217

RESULT 3  
 US-08-589-028-10  
 Sequence 10: Application US/0859028  
 Patent No. 6091290

GENERAL INFORMATION:  
 INVENTOR: Neogard, Christopher B.  
 APPLICANT: Halban, Philippe  
 APPLICANT: No. 6081290/Canada, Karl D.  
 APPLICANT: Thigpen, Antie B.  
 APPLICANT: Canada, Christian  
 TITLE OF INVENTION: Precombiant Expression of Proteins from  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Neogard, Christopher B.  
 ADDRESS: P. O. Box 4433  
 CITY: Houston  
 STATE: TX

COUNTRY: USA  
 ZIP: 77210-4433  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Pictent Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/08/589,028  
 FILING DATE: Concurrently Herewith

CLASSIFICATION: 415  
 PRIOR APPLICATION NUMBER: 08/199,060  
 FILING DATE: February 4, 1994  
 CLASSIFICATION: 415  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 47,642  
 REFERENCE/DOCKET NUMBER: 07/426/HNL  
 TELECOMMUNICATIONS: 612 418-3000  
 TELEFAX: (612) 474-7577

INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 217 amino acids  
 TYPE: amino acid  
 STRANDS: linear  
 US-08-589-028-10

Query Match 97.9% Score 1024.5; DB 3; Length 217;  
 Best Local Similarity 92.7% Pred. No. 7.2e-108;  
 Matches 201: Conservative 1, Mismatches 1, Indels 15, Gaps 1;  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 60  
 1 MATGSRFTLLAFGLCLPWAGSSAPFTTPTLRFPNMSIARHQLADPTQFEKA 63  
 58 -----NPGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 105  
 61 YIPKQVYFYLQNGTLCPSRSPSPNNEETQKSNELASILLIQMELPVQELA 120







Tue Feb 8 14:23:52 2005

DB 1 MA6SRISLLAFGLCLSMWQKESAFPTTJSLPDMALNHRHQLAQPTQSFREA 60  
 58 -----APQTSCTSPSSPPSPSRRETOXSNELTSLTLLQMGAPROPR 105  
 DB 61 YTPKESQFLQFQVGLQGLQVLRSSPPSRNRRQVSNELTSLTLLQMGAPROPR 120  
 106 SPVANSVLVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 165  
 DB 121 VYDNLALVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 180  
 161 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 202  
 DB 181 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 217

RESULT 11

US-09-411-657-4  
 Application US/09411657

Patent No. 656628

GENERAL INFORMATION: 6  
 APPLICANT: INVENTION: Human Growth Factor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: 7  
 ADDRESS: 3410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 09/09/411,657  
 FILING DATE: 09/09/411,657

CLASSIFICATION: 6  
 PRIOR APPLICATION DATA:  
 PRIORITY NUMBER: 06/710,324

ATTORNEY/AGENT INFORMATION:  
 NAME: BROOKER, A. ANDER  
 ADDRESS: 373  
 TELEPHONE: 01-01-3628304

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 01-01-3628304

SEQUENCE CHARACTERISTICS:  
 INFORMATION FOR SEQ ID NO: 4:  
 LENGTH: 217 AMINO ACIDS  
 STRANDNESS: ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-09-411-657-4

Query Match 97.1%; Score 1016.5; DB 4; Length 217;  
 Best Local Similarity 97.0%; Gaps 1;  
 Matches 209; Conservative 2; Indels 15; Gaps 1;

DB 1 MATSRTSLLAFLCLCLWLGNSPPTTJSLPDMALNHRHQLAQPTQSFREA 60  
 58 -----APQTSCTSPSSPPSPSRRETOXSNELTSLTLLQMGAPROPR 105  
 DB 61 YTPKESQFLQFQVGLQGLQVLRSSPPSRNRRQVSNELTSLTLLQMGAPROPR 120  
 106 SPVANSVLVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 165  
 DB 121 VYDNLALVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 180  
 161 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 202  
 DB 181 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 217

DB 166 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 202  
 DB 181 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 217

RESULT 12  
 US-08-187-756C-5  
 Application US/08187756C

Sequence 5: APPLICATION: Human Growth Hormone

GENERAL INFORMATION: 6  
 APPLICANT: ROSEN, ET AL.

TITLE OF INVENTION: Human Growth Hormone

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: 7  
 ADDRESS: CARLEA, ERNEST, BAY CITY, ILL.  
 ADDRESS: BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA: 08/187,756C  
 FILING DATE: January 27, 1994

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 PRIORITY NUMBER:

ATTORNEY/AGENT INFORMATION:  
 NAME: PERANO, GREGORIO  
 ADDRESS: 6134  
 TELEPHONE: 201-943-7744

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-943-7744

SEQUENCE CHARACTERISTICS:  
 INFORMATION FOR SEQ ID NO: 5:  
 LENGTH: 198 AMINO ACIDS  
 STRANDNESS: ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-187-756C-5

Query Match 95.4%; Score 999; DB 1; Length 198;  
 Best Local Similarity 97.0%; Gaps 1;  
 Matches 196; Conservative 2; Indels 15; Gaps 1;

DB 1 MATSRTSLLAFLCLCLWLGNSPPTTJSLPDMALNHRHQLAQPTQSFREA 60  
 58 -----APQTSCTSPSSPPSPSRRETOXSNELTSLTLLQMGAPROPR 105  
 DB 61 YTPKESQFLQFQVGLQGLQVLRSSPPSRNRRQVSNELTSLTLLQMGAPROPR 120  
 106 SPVANSVLVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 165  
 DB 121 VYDNLALVYQASNSHNVDTLLDEBQITQMLNIDNSPTQJFQVTSKFTNSHND 180  
 161 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 202  
 DB 181 ALNRYVGLACRDMKQKVFETPLAVQCSVSSQCF 217

RESULT 13  
 US-08-710-324A-5

Sequence 5, Application US/08710324A  
 Patent No. 5962411  
 INVENTOR: ROSEN, RAYMOND  
 APPLICANT: ROSEN, RAYMOND  
 TITLE OF INVENTION: Human Growth Factor  
 NUMBER OF SEQUENCES: 7  
 INVENTOR'S ADDRESS: Human Genome Sciences, Inc.  
 ADDRESS: 10000 Rockville Pike  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/08710324A  
 APPLICATION NUMBER: US/08/710,324A  
 FILING DATE: 16-SEP-1996  
 PRIORITY DATE: 435  
 CLASSIFICATION: 373  
 REFERENCE NUMBER: 373  
 ATTORNEY/AGENT INFORMATION:  
 FILING DATE: 27-JAN-1994  
 REFERENCE NUMBER: 373  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8439  
 TELEFAX: 301-309-8439  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: AMINO ACID  
 STRAND: STRAND  
 MOLECULE TYPE: PROTEIN  
 US-08-710-324A-5

Query Match 95.4%; Score 999; DB 2; Length 198;  
 Best Local Similarity: 97.0%; Pred. No. 4.9e-105;  
 Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;  
 Db 1 MANGERSILLAPFLLCQWQSGSAPPTPLSPFNNSAARHQAQVLTPTGEPNG 60  
 Db 1 MANGERSILLAPFLLCQWQSGSAPPTPLSPFNNSAARHQAQVLTPTGEPNG 60  
 Db 61 TSLCTRESPTPSNREYTOQSNELRLISLLIQSLPEVPTASVNNVLYGASNS 120  
 Db 58 -SLCTRESPTPSNREYTOQSNELRLISLLIQSLPEVPTASVNNVLYGASNS 116  
 Db 121 VYLLAKNLEGIQTLMRLECSPPVQIQKQYKEDPTNSNDLALNYGLCYFRND 180  
 Db 117 VYLLAKNLEGIQTLMRLECSPPVQIQKQYKEDPTNSNDLALNYGLCYFRND 176  
 Db 181 MGVETFLAPVCHVSGSCIP 302  
 Db 177 MGVETFLAPVCHVSGSCIP 198

RESULT 14  
 US-09-411-657-5  
 Sequence 5, Application US/09411657  
 INVENTOR: ROSEN, RAYMOND  
 APPLICANT: ROSEN, RAYMOND  
 TITLE OF INVENTION: Human Growth Factor  
 NUMBER OF SEQUENCES: 7  
 INVENTOR'S ADDRESS: Human Genome Sciences, Inc.  
 ADDRESS: 10000 Rockville Pike  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850

CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/09411,657  
 APPLICATION NUMBER: US/09/411,657  
 FILING DATE: 08/710,324  
 PRIORITY DATE: 435  
 CLASSIFICATION: 373  
 REFERENCE NUMBER: 373  
 ATTORNEY/AGENT INFORMATION:  
 FILING DATE: 27-JAN-1994  
 REFERENCE NUMBER: 373  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8439  
 TELEFAX: 301-309-8439  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: AMINO ACID  
 STRAND: STRAND  
 MOLECULE TYPE: PROTEIN  
 US-09-411-657-5

Query Match 95.4%; Score 999; DB 4; Length 198;  
 Best Local Similarity: 97.0%; Pred. No. 4.9e-105;  
 Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;  
 Db 1 MANGERSILLAPFLLCQWQSGSAPPTPLSPFNNSAARHQAQVLTPTGEPNG 60  
 Db 1 MANGERSILLAPFLLCQWQSGSAPPTPLSPFNNSAARHQAQVLTPTGEPNG 60  
 Db 61 TSLCTRESPTPSNREYTOQSNELRLISLLIQSLPEVPTASVNNVLYGASNS 120  
 Db 58 -SLCTRESPTPSNREYTOQSNELRLISLLIQSLPEVPTASVNNVLYGASNS 116  
 Db 121 VYLLAKNLEGIQTLMRLECSPPVQIQKQYKEDPTNSNDLALNYGLCYFRND 180  
 Db 117 VYLLAKNLEGIQTLMRLECSPPVQIQKQYKEDPTNSNDLALNYGLCYFRND 176  
 Db 181 MGVETFLAPVCHVSGSCIP 302  
 Db 177 MGVETFLAPVCHVSGSCIP 198

RESULT 15  
 US-09-411-657-5  
 Sequence 5, Application US/09411657  
 INVENTOR: ROSEN, RAYMOND  
 APPLICANT: ROSEN, RAYMOND  
 TITLE OF INVENTION: Human Growth Factor  
 NUMBER OF SEQUENCES: 7  
 INVENTOR'S ADDRESS: Human Genome Sciences, Inc.  
 ADDRESS: 10000 Rockville Pike  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850

STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER RELEASABLE ROOM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Recent in Release #1.0, Version #1.30  
 CONSOLE: IBM PC compatible  
 APPLICATION NUMBER: US/08/784,582  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA: US 60/028,427  
 FILING DATE: 15-OCT-1996  
 PRIOR APPLICATION DATA: US 08/589,028  
 FILING DATE: 19-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haglund, Steven L.  
 REFERENCE/DOCKET NUMBER: 43,642  
 TELEPHONE: 512/419,000  
 TELEFAX: 512/443,700  
 TELECOMMUNICATION INFORMATION:  
 INFORMATION FOR SEQ ID NO: 73:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 360 amino acids  
 STRANDNESS: 1  
 TOPOLOGY: linear  
 US-08-784-582-73

Query Match 88.5%; Score 926.5; DB 3; Length 360;  
 Best Local Similarity 87.6%; Seed No. 26-96; 7; Indels 15; Gaps 1;  
 Matches: 184; Connective 4; Mismatches 7;

Oy 1 VQTSRSTLLAPRLCPPTLRQNSAPPTPLSLRLTNSLRANHLNQLPTPTQSR-- 57  
 1 MATSRSTLLANGLCLAPRLQSSAPPTPLSLRLTNSLRANHLNQLAPPTQSR 60  
 Oy 58 -----NQTSICPSSESPPTSPREFTQSNELRLSLISGLISGRL 105  
 61 YIPKQKTSFCLQPTSLCSSESPPTSPREFTQSNELRLSLISGLISGRL 120  
 Oy 106 SYFANSLVQASDSNVDLKLDSQQTTLNHLNLSPTTQITPTYSSTGNSND 165  
 121 SYFANSLVQASDSNVDLKLDSQQTTLNHLNLSPTTQITPTYSSTGNSND 180  
 Oy 166 ALNPNGLVCFKQKQNTFFATVQRS 195  
 181 ALNPNGLVCFKQKQNTFFATVQRS 210  
 DB

Search completed: February 6, 2005, 13:06:01  
 Job time : 44 secs









101 VALDIAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 120  
 361 GCTATGAGCCCTTAAAGAGCTATGAGAGAGCTGACCAAGCTGATGGAGCTGAA 420  
 121 VAIYVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAP 140  
 421 GATGACACCCCTGAGATGAGCTGATGATGATGATGATGATGATGATGATGAT 480  
 141 AAGVYSEPTDITDITDITDITDITDITDITDITDITDITDITDITDITDITDIT 160  
 481 TCGACACACATATGACATGATGATGATGATGATGATGATGATGATGATGAT 540  
 161 SEHIAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 180  
 541 ATGAGACAGCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 181 MCHVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAP 200  
 601 GAGCTTC 606  
 201 GYPha 202

RESULT 4  
 AAR60516 standard; protein: 217 AA.  
 AAR60516:  
 AAR60516: 25-MAR-2003 (revised)  
 DT 22-MAR-1995 (first entry)

Human gonatotrophin.  
 Serine protease; factor-Xa; recognition site; fusion protein cleavage;  
 protein folding; growth hormone (growth hormone); growth hormone  
 polymerase chain reaction; amplification.  
 OS Homo sapiens.  
 OS M0941827-42.  
 18-AUG-1994.  
 04-FEB-1994; 94MO-D0000054.  
 04-FEB-1993; 93DC-00000130.  
 05-FEB-1993; 93MO-00000130.  
 03-DEC-1993; 93MO-00000130.  
 (DENZ-) DENZYME ASS.  
 Thogreen HC, Hollet TL, Ezerodt M;  
 WPI, 1994-739681/34.  
 Refolding of polypeptide molecules - using a cyclic process involving  
 denaturing and renaturing conditions to produce a correctly folded prod.

Disclaimer: Page 129-130, 202pp. English.

cDNA encoding human gonatotrophin (a sequence given in AAR60516) was PCR  
 amplified using primers given in AAR60516. The cDNA was then linked  
 to a sequence encoding a factor-Xa recognition site (given in AAR60516).  
 The resulting fusion protein was expressed in E. coli (JM103) and  
 purified using a factor-Xa recognition site. The purified protein was  
 refolded using a cyclic process involving denaturing and renaturing  
 conditions to obtain a correctly folded recombinant protein.  
 Updated on 25-MAR-2003 to correct PW field.)

Sequence 217 AA:  
 SQ

Alignment Scores:  
 Score: 5,286.99 Length: 217  
 Percent Similarity: 1029.50 Matches: 202  
 Best Local Similarity: 93.08 Mismatches: 15  
 Identical: 92.58  
 Gaps: 1

US-95-856-796D-1 (1-609) x AAR60516 (1-217)

1 ATGCTGACAGCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 60  
 1 MCHVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAP 20  
 61 CTTCGACACATATGACATGATGATGATGATGATGATGATGATGATGATGAT 120  
 21 LEADAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 40  
 121 CTTCGACACATATGACATGATGATGATGATGATGATGATGATGATGATGAT 171  
 41 LEADAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 60  
 171 ----- ACCGACACCCCTGAGATGAGCTGATGATGATGATGATGATGAT 195  
 61 Tyrtieroyseidulidyltyserphenylamperidolthiesteracylpyr 255  
 196 TCGACACATATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 315  
 81 SEHIAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 400  
 256 CTTCGACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 460  
 101 LEADAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 520  
 316 AGCTGCTTCGACATGATGATGATGATGATGATGATGATGATGATGATGAT 575  
 121 SEHIAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 640  
 376 AAGACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695  
 141 LEADAHNSHVSSEVSLFHALLAHMSERLAVLYTGIYALASERASERAN 760  
 436 ACTGACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815  
 161 THOGVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAP 880  
 496 GDCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 945  
 181 AAGVYSEPTDITDITDITDITDITDITDITDITDITDITDITDITDITDITDIT 1000  
 556 AATTCCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1055  
 201 THOGVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAP 1110

RESULT 5  
 AAR60516 standard; protein: 217 AA.  
 AAR60516:  
 AAR60516: 12-MAR-2002 (first entry)  
 DT 12-MAR-2002 (first entry)

Growth hormone 1 gene (GHI), 859L mutant.  
 Growth hormone 1 (GHI); osteoporosis; gene therapy; protein therapy;  
 diabetes; obesity; infection; acromegaly; gigantism; sleep disorder;  
 water retention; metabolic storage; growth hormone deficiency;  
 growth hormone; growth hormone; growth hormone; growth hormone;  
 those features pituitary storage defect; human; mutant.  
 Homo sapiens.  
 Synthetic.

Sequence 217 AA:  
 SQ



D<sub>B</sub> 141 LysAspSplEuglIucIYleGlnThrMetGlyArgSplLysPheProArg 160

436 ACTIVATION OF THE CYP1A1 GENE BY

[illegible]

	Location: K08679
key	56
Misc-difference	/notes= "wild type Glu substituted by Gly"
PT	
FT	

XX	WO20018593-A2.
PN	
XX	
PD	15-NOV-2001.

XX 14-MAY-2001; 2001MO-GB002126.  
PF  
XX

```
PR 12-MAY-2000; 2000GB-00011459;
PR 14-JUL-2000; 2000EP-00306004.
```

AA  
PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
XX

PI	Cooper DN, Procter AM, Gregory J, Miller USJ
XX	
nn	DOI: 10.1002/088798/12

XX in screening patients for

PT Detecting growth hormone variants (GH/V), useful in screening patients with growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard

PT sequence of the human GHI.

xx The invention described a method of detecting variation in growth hormone  
cc Claim 20; Fig. 1; 50pp; engraving.

1 (GH1), and therefore GH dysfunction in an individual. The method  
CC 1 (GH1), and therefore GH dysfunction in an individual. The method  
CC comprises comparing the nucleotide sequence of GH1 gene obtained from the  
CC individual with a standard human GH1 gene sequence, in order to identify

test fragile with a statistically normal and good correlation with variation (GHI variant). The method is useful in screening patients for growth hormone irregularities or producing variant proteins for treating

irregularities, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in management of clinical or detection method, particularly for determining absence of diagnostic or detection method, particularly for determining

CC **inherently, regardless of whether**  
CC **binding defects and susceptibility to a disease such as diabetes, obesity**  
CC **or infection; for treating acromegaly or gigantism conditions associated**  
CC **with growth hormone secretagogue receptor effects.**

CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects.













The invention described a method of detecting variation:

The invention described a method of detecting variation in growth hormone



















Tue Feb 8 14:23:46 2005

us-09-856-796b-1.rtf

Page 7

[illegible][illegible][illegible]

RESULT 10 32  
Sequence 4  
Patent No. 5965411  
GENERAL INFORMATION:  
TITLE OF INVENTION: et al  
NUMBER OF INVENTORS: 7  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
STREET: 9410 Katy West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
COMPUTER TYPE: floppy disk  
COMPUTER NAME: PC-XT/286  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
APPLICATION NUMBER DATA:  
APPLICATION NUMBER DATA: 068/710,344  
FILING DATE: 16-SEP-1996  
PRIORITY DATA:  
PRIORITY NUMBER DATA: 435  
PRIORITY DATE: 27-JAN-1994  
APPLICATION NUMBER: US 08/187,766  
FILING DATE: 27-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: [REDACTED]  
FIRM: [REDACTED]  
REGISTRATION NUMBER: 36,373



Tue Feb 8 14:23:46 2005

us-09-856-796b-1.rtf

Page 9

[illegible][illegible]





[illegible]

***This Page Blank (uspio)***

























[illegible]

PN	JP 198044990-A/1
PD	06-OCT-1986
PF	29-MAR-1985 JP 1985066208
PI	NAKAJIMA KUNIO, NAGAI JUN
PC	C12N15/00//C12P21/02, (C12N15/00, C12R1:19)

















Oy 316 AGTGTCTTGCGCAACAGCTGGTATACGGGCGCTTGTACACACACGATCATGACTCTTA 375  
Db 361 AGTGTCTTGCGCAACAGCTGGTATACGGGCGCTTGTACACACACGATCATGACTCTTA 420  
Oy 376 AAGGACCTAGAGAGAAAGGACCTCAAAGCTGTATGAGGAGATGCAAGCCCGG 435  
Db 421 AAGGACCTAGAGAGAGGACCTCAAAGCTGTATGAGGAGATGCAAGCCCGG 480  
Oy 436 AATGGGCAATCTTCAAGCACTTACACGATTCGACCAAGCTGACCAACGATGAC 495  
Db 481 ACTGGGCAATCTTCAAGCACTTACACGATTCGACCAAGCTGACCAACGATGAC 540  
Oy 496 GCACTACTCAAGACTACGGGCTGCTTACTGCTTACGAGAGACATGACAAAGTTCAG 555  
Db 541 GCACTACTCAAGACTACGGGCTGCTTACTGCTTACGAGAGACATGACAAAGTTCAG 600  
Oy 556 ACATTCTGACGATGTCGACGTCGCTCTCTGTGAGAGGACCTGTGGCTTTAG 609  
Db 601 ACATTCTGACGATGTCGACGTCGCTCTCTGTGAGAGGACCTGTGGCTTTAG 654

Search completed: February 7, 2005, 11:39:58  
Job Time : 3093 secs































**This Page Blank (uspio)**

















STREET: George Mason Bldg., Washington & Prince Sts.  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM: 414b  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 APPLICATION NUMBER: US-08-117-809A  
 FILING DATE: 09-SEP-1993  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: JP 240936/1992  
 FILING DATE: 09-SEP-1992  
 PRIORITY APPLICATION DATA: JP 009911/1993  
 FILING DATE: 25-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crane Peury, Sharon E.  
 REFERENCE/DOCKET NUMBER: 029430-163  
 TELEPHONE: (703) 835-6520  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 859 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 ORGANISM: Bacillus anthracis  
 STRAIN: Mt-272  
 FEATURES: key: CDS  
 LOCATION: 251..859  
 FEATURES: key: misc feature  
 LOCATION: 171..272  
 OTHER INFORMATION: /note= "Nucleotide 179-208 are S  
 REGION INFORMATION: promoter."  
 FEATURES: key: sds region  
 LOCATION: 251..331  
 FEATURES: key: RBS  
 LOCATION: 236..242  
 FEATURES: key: mat\_peptide  
 LOCATION: 332..859  
 US-08-117-809A-1

Query Match 82.2% Score 500.6; Db 1; Length 859;  
 Match Local similarity 76.4% Fred. No. 1.1e-138  
 Matches 512; Conservative 19; Indels 0; Gaps 0;

76 GCTCTCCACCACTCTCTCTTCAACGCTTTTTCACAGCTAGCTCCGCCCACTCGT 135  
 139 GCTCTCCACCACTCTCTCTTCAACGCTTTTTCACAGCTAGCTCCGCCCACTCG 388  
 136 CTCTCAACGCTCTCTTCAACGCTTTTTCACAGCTAGCTCCGCCCACTCTCTTC 195  
 389 CTCTCAACGCTCTCTTCAACGCTTTTTCACAGCTAGCTCCGCCCACTCTCTTC 448  
 136 TCGAGCTTATCTTCAACGCTCTTCAACGCTAGGAGAAACGACGAGAAATTCAGT 255  
 449 TCGAGCTTATCTTCAACGCTCTTCAACGCTAGGAGAGAGAGAGAGAGAGAGAG 508  
 256 CTGCTCCCACTCA 315

Db  
 508 CTGCTCCCACTCA 568  
 316 AGCT 775  
 569 AGCT 828  
 316 AGCT 885  
 629 AGCT 888  
 436 AGCT 945  
 689 AGCT 948  
 496 GAGCT 955  
 749 GAGCT 908  
 556 AGCT 966  
 809 AGCT 959

RESULT 13  
 US-08-117-809A-2

Sequence 2, Application US/08117809A  
 GENERAL INFORMATION:  
 APPLICANT: HONOLULU, Hawaii  
 APPLICANT: YOSHINO, Susuo  
 APPLICANT: YOSHINO, Susuo  
 APPLICANT: NAITO, Nobuaki  
 TITLE OF INVENTION: PROCESS FOR PRODUCTION OF HUMAN GROWTH  
 HORMONE  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Burns, Doane, Specker & Mathis  
 STREET: George Mason Bldg., Washington & Prince Sts.  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM: 414b  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 APPLICATION NUMBER: US-08-117-809A  
 FILING DATE: 09-SEP-1993  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: JP 240936/1992  
 FILING DATE: 09-SEP-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 009911/1993  
 FILING DATE: 25-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Crane Peury, Sharon E.  
 REFERENCE/DOCKET NUMBER: 029430-163  
 TELEPHONE: (703) 835-6520  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 859 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 ORGANISM: Bacillus anthracis  
 STRAIN: Mt-272  
 ORIGINAL SOURCE:



Oy 496 GCACTATCAAGAAATACAGGAGCTCTATCTCTTCCAGAGAAACATGACGAAAGCTCGAG 555  
 Db 541 GCACTGCTCAAGAAATACAGGAGCTCTATCTCTTCCAGAGAAACATGACGAAAGCTCGAG 600  
 Oy 556 AACTTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 609  
 Db 601 AACTTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 654

## RESULT 15

US-08-710-324-1

Patent No. 5962411

GENERAL INFORMATION:

APPLICANT: Roman, et al.

INVENTOR: Human Growth Factor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

CITY: Rockville

STATE: MD

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CLASSIFICATION: 435-1596

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/187,756

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8504

IMPROVEMENTS: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 654 base pairs

TYPE: nucleic acid

STRANDS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-710-324-1

Query Match 81.0% Score 493.2; DB 2; Length 654;  
 Best Local Similarity 87.3%; Pred. No. 1.5e-136; Indels 45; Gaps 1;  
 Matches 571; Conservative 0; Mismatches 38;

Db 241 TCAAGATCTATTCAGAACTCTCCAGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 Oy 256 CTGCTCCGCACT 315  
 Db 301 CTGCTCCGCACT 360  
 Oy 316 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 375  
 Db 361 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 420  
 Oy 376 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 435  
 Db 421 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 480  
 Oy 436 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 495  
 Db 481 AAGTCTTCTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 540  
 Oy 496 GCACTATCAAGAAATACAGGAGCTCTATCTCTTCCAGAGAAACATGACGAAAGCTCGAG 555  
 Db 541 GCACTGCTCAAGAAATACAGGAGCTCTATCTCTTCCAGAGAAACATGACGAAAGCTCGAG 600  
 Oy 556 AACTTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 609  
 Db 601 AACTTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTTCCAGAGCTCTATCTCTT 654

Search completed: February 7, 2005, 12:30:44  
 Job time : 166 secs





















```

Db      161 CTCGCGCCGCCATCGTCGACACGCTGGCTTTGACCTACAGAGATTGGAAGAGCC 220
Qy      172 -----AACCCGAGAGCTGCTCTGTGTTG 195
Db      221 TATATCCAGAGAGACAGAGATTTATCTTCGCGAGACCCCGAGAGCTGCTGTGTTTC 280
Qy      196 TCGAGATCTATTCGACACCTTCGACAGGAGAGAGAACACAGAGAAATCGAACTAGAG 255
Db      281 TCGAGATCTATTCGACACCTTCGACAGGAGAGAGAACACAGAGAAATCGAACTAGAG 340
Qy      256 CTGCTCCGATTTCCCTGCTGCTCATCGATCGTGGTGGAGCCGATTCGATGCTCAAG 315
Db      341 CTCGCGCGATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 400
Qy      316 AGTGTCTTCGACACAGCTGATGTGATGAGGAGGCTCTGACAGCAAGATCTATGACTCTA 375
Db      401 AGTGTCTTCGACACAGCTGATGTGATGAGGAGGCTCTGACAGCAAGATCTATGACTCTA 460
Qy      376 AAGGACTTGAAGAGAGAGGATCTCAAGAGCTGATGGAGAGGCTGGAGAAATGGACCCCGG 435
Db      461 AAGGACTTGAAGAGAGAGGATCTCAAGAGCTGATGGAGAGGCTGGAGAAATGGACCCCGG 520
Qy      435 ACTGGGAGATCTTCAGAGCACTGACAGCAAGATGGAGAAATGGACCAAGATGAG 495
Db      521 ACTGGGAGATCTTCAGAGCACTGACAGCAAGATGGAGAAATGGACCAAGATGAG 580
Qy      496 GCACTACTGAGAAAGATGAGAGGCTGCTTACTGCTTCAAGAAAGGACATGACAGAGTCAAG 555
Db      581 GCACTACTGAGAAAGATGAGAGGCTGCTTACTGCTTCAAGAAAGGACATGAGAGGTCAG 640
Qy      556 AACTTTCTTGGCATCTGTCAGATGTCGCTCTGATGAGAGGAGCACTGATGCTCTTCA 609
Db      641 AACTTTCTTGGCATCTGTCAGATGTCGCTCTGATGAGAGGAGCACTGATGCTCTTCA 694

```

Search completed: February 7, 2005, 13:39:05  
 Job time : 482 sec















Db	141	lyv#pserlndubdly11edntlmawerpragndubagolyserfackg	160
Qy	436	ATGGGCGATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	495
Db	161	thrdlynlstlephelygelntlyserfserphesaprlatasecrlanmapap	180
Qy	496	GACATCTGATGAACTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	555
Db	181	serdelmduyenytycdylmelnthwphesaprlatasecrlanmapap	200
Qy	556	ACATCTGACATGACATGACATGACATGACATGACATGACATGACATG	606
Db	201	thrphealngthvnlacdyserpnlavldublysercydolyse	217
RESULT 8			
167411			
somatotropin - rhesus macaque			
C:Species: Homo sapiens (man)			
C:Date: 30-Jun-1998 Sequence revision 30-Jun-1998 #rec_change 09-Jul-2004			
C:Release: 31-May-1996 Sequence revision 31-May-1996 #rec_change 09-Jul-2004			
C:Accession: 167411			
C:Release: 31-May-1996 Sequence revision 31-May-1996 #rec_change 09-Jul-2004			
A:Title: Cloning of four growth hormone/chorionic somatomotropin-related complementary			
A:Reference number: 153257; MID: 9408724; PMID: 8404617			
A:Release: 13-Nov-1994 Sequence revision 13-Nov-1994 #rec_change 09-Jul-2004			
A:Status: preliminary; translated from GR/GEN/DBD			
A:Molecule type: mRNA			
A:Release: 1-217 <S>			
C:Superfamily: prolactin			
C:Superfamily: prolactin			
Alignment Scores:			
Pred. No.: 1			
Score: 843.50			
Percent Similarity: 82.95%			
Best Local Similarity: 76.50%			
Query Match: 2-63%			
DB: 1			
US-09-856-796b-1 (1-609) 3 167411 (1-217)			
Qy	1	ATGGGCGATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	60
Db	1	MECHALADYSETRTHYVGLNLELALALALALALALALALALALALALAL	20
Qy	61	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	120
Db	21	LAUHLIDUVALDYALVALINDHLYPRLSESRFGLVLPRLAPRLALALAL	40
Qy	121	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	171
Db	41	PHKATGALHIALHIALHIALHIALHIALHIALHIALHIALHIALHIALH	60
Qy	172	ACCCGACATCTTTCACAGCTGACCTGACATGACATGACATGACATG	195
Db	172	TYRLEPGLYDELINLYTYRSEPRHLYLGLALGRLINLHLSERFHYE	80
Qy	196	TGACATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	255
Db	81	SERLESETRFOTHPROSEHLESLINDHLYPRLSESRFGLVLPRLAP	100
Qy	256	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	315
Db	101	LAUHLIDUVALDYALVALINDHLYPRLSESRFGLVLPRLAPRLALAL	120
Qy	316	ACATCTGACATGACATGACATGACATGACATGACATGACATGACATG	375
Db	121	SERLEPRLALHIALHIALHIALHIALHIALHIALHIALHIALHIALH	140
Qy	376	ACCCGACATCTTTCACAGCTGACCTGACATGACATGACATGACATG	435

Db	141	lyv#pserlndubdly11edntlmawerpragndubagolyserfackg	160
Qy	436	ATGGGCGATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	495
Db	161	thrdlynlstlephelygelntlyserfserphesaprlatasecrlanmapap	180
Qy	496	GACATCTGATGAACTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	555
Db	181	serdelmduyenytycdylmelnthwphesaprlatasecrlanmapap	200
Qy	556	ACATCTGACATGACATGACATGACATGACATGACATGACATGACATG	606
Db	201	thrphealngthvnlacdyserpnlavldublysercydolyse	217
RESULT 9			
167449			
chorionotropin precursor (allele hC-3) - human			
C:Species: Homo sapiens (man)			
C:Date: 30-Jun-1998 Sequence revision 30-Jun-1998 #rec_change 09-Jul-2004			
C:Release: 31-May-1996 Sequence revision 31-May-1996 #rec_change 09-Jul-2004			
C:Accession: 167449			
A:Title: The human growth hormone gene locus, structure, evolution, and allelic variatio			
A:Reference number: 153257; MID: 9408724; PMID: 8404617			
A:Release: 13-Nov-1994 Sequence revision 13-Nov-1994 #rec_change 09-Jul-2004			
A:Status: preliminary; translated from GR/GEN/DBD			
A:Molecule type: DNA			
A:Release: 1-217 <S>			
C:Superfamily: prolactin			
C:Superfamily: prolactin			
Alignment Scores:			
Pred. No.: 2			
Score: 83.41%			
Percent Similarity: 77.88%			
Best Local Similarity: 75.76%			
Query Match: 2			
DB: 3			
US-09-856-796b-1 (1-609) 3 167449 (1-215)			
Qy	1	ATGGGCGATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	60
Db	1	MECHALADYSETRTHYVGLNLELALALALALALALALALALALALALAL	20
Qy	61	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	120
Db	21	LAUHLIDUVALDYALVALINDHLYPRLSESRFGLVLPRLAPRLALALAL	40
Qy	121	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	171
Db	41	PHKATGALHIALHIALHIALHIALHIALHIALHIALHIALHIALHIALH	60
Qy	172	ACCCGACATCTTTCACAGCTGACCTGACATGACATGACATGACATG	195
Db	172	TYRLEPGLYDELINLYTYRSEPRHLYLGLALGRLINLHLSERFHYE	80
Qy	196	TGACATCTTTCACAGCTGACCTGACATGACATGACATGACATGAC	255
Db	81	SERLESETRFOTHPROSEHLESLINDHLYPRLSESRFGLVLPRLAP	100
Qy	256	CTTCAAGGCGATCTTTCACAGCTGACCTGACATGACATGACATGAC	315
Db	101	LAUHLIDUVALDYALVALINDHLYPRLSESRFGLVLPRLAPRLALAL	120
Qy	316	ACATCTGACATGACATGACATGACATGACATGACATGACATGACATG	375
Db	121	SERLEPRLALHIALHIALHIALHIALHIALHIALHIALHIALHIALH	140
Qy	376	ACCCGACATCTTTCACAGCTGACCTGACATGACATGACATGACATG	435
Db	139	lyv#pserlndubdly11edntlmawerpragndubagolyserfackg	158

436 ACTGCGAGATCTTCAGAGACGACCTACAGCAATTCACACAACTACACCAATAC 495  
 159 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178  
 496 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555  
 179 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 198  
 556 AACTTCTGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606  
 199 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 215

## RESULT 10

167408 *gataa2* (gataa2:rat) - 3 - chusn sequence (fragment)  
 CSpecies: Musca musca  
 CDate: 31-May-1996 Requery: revision 31-May-1996 Exec: Change 09-Jul-2004  
 CAccession: 167408  
 CAccession: 167408 M. Fisher, J.M. Poirier, P.D.  
 Biotechnology 133744-1155, 1993  
 ATitle: Cloning of four growth hormone/chorionic gonadotropin-related complement  
 AReference number: 133745; NID:35008724; PMID:8404617  
 AAccession: B32435  
 AStatus: preliminary  
 ASpecies: preliminary; translated from GB/BBM/DOB  
 AReference type: mRNA  
 AAccession: 1-212 -CHS-  
 CSpecies: preliminary; translated from GB/BBM/DOB  
 CSpecies: preliminary; translated from GB/BBM/DOB

Alignment Scores:  
 Score: 1,776-61 Length: 212  
 Percent Similarity: 83.150 Matches: 160  
 Basic Local Similarity: 83.965 Conservative: 18  
 Query Match: 74.478 Mismatches: 13  
 Dp: 2 Gaps: 1

US-09-856-796b-1 (1-609) x 167408 (1-212)

16 GCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75  
 Db 1 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20  
 76 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135  
 Db 21 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 40  
 136 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 171  
 Db 41 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60  
 172 -----AACCCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 210  
 Db 61 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 80  
 211 AACTCTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370  
 Db 81 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 100  
 271 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310  
 Db 101 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 331 AACTCTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 390  
 Db 121 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 140  
 391 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450  
 Db 141 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 160  
 451 AACTCTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510

Db 161 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 511 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 570  
 Db 181 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 200  
 571 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606  
 Db 201 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 212

## RESULT 11

832435 *choxiomamotrogin-like protein precursor - human*  
 CSpecies: Homo sapiens (man)  
 CAccession: 832435  
 CDate: 09-Dec-1989 Requery: revision 29-Dec-1989 Exec: Change 09-Jul-2004  
 CAccession: 832435  
 RChen, B.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Salzman, H.A.; Gelman, R.; Seeburg, P.J.  
 Genes 4, 479-497, 1989  
 ATitle: The human 92kD human lung; nucleotide sequence, biochemistry, and evolution.  
 AReference number: 832435; NID:86307277; PMID:2744760  
 AAccession: B32435  
 AStatus: preliminary  
 ASpecies: preliminary  
 AAccession: 1-199 -CHS-  
 CSpecies: preliminary; translated from GB/J03071; NID:9183148; PMID:52550.1; PID:9183150  
 CSpecies: preliminary; translated from GB/J03071; NID:9183148; PMID:52550.1; PID:9183150

Alignment Scores:  
 Score: 3,856-57 Length: 199  
 Percent Similarity: 77.950 Matches: 157  
 Basic Local Similarity: 77.128 Conservative: 32  
 Query Match: 70.104 Indels: 1  
 Dp: 2 Gaps: 1

US-09-856-796b-1 (1-609) x B32435 (1-199)

1 ATGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
 Db 1 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20  
 61 CTTCACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 21 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 40  
 121 CTTCACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 Db 41 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60  
 181 ACCTCTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 Db 61 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 77  
 241 AACTCTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 Db 78 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 97  
 301 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 Db 98 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 117  
 361 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 Db 118 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137  
 421 GCGCTACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 Db 138 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 157  
 481 CTTCACCAAGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 158 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 177









***This Page Blank (uspto)***

























***This Page Blank (uspio)***































***This Page Blank (uspto)***